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OM protein - protein search, using sw model

Run on: January 26, 2006, 12:29:46 ; Search time 74 Seconds

(without alignments)
362.191 Million cell updates/sec

Title: US-09-980-672-2

Perfect score: 342
Sequence: 1 SHLVKCAKEKTEFCVNGSEC.....GDRCONVMA5FYAAELIYQ 61

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 1199344

Minimum DB seq length: 0
Maximum DB seq length: 61

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the change being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	342	100.0	61	8	AD45192 Human neu
2	342	100.0	61	8	AD509196 Human neu
3	342	100.0	61	8	AD52008 Recombina
4	342	100.0	61	8	AD28541 Human neu
5	337	98.5	60	2	AA55660 EGFL3. 3/
6	337	98.5	60	2	AA46919 EGFL3. 3/
7	337	98.5	60	2	AA67251 Human epi
8	337	98.5	60	2	AA96077 Epidermal
9	337	98.5	60	2	AA09364 Epidermal
10	337	98.5	60	2	AA87462 Epidermal
11	316	92.4	58	3	AA12601 Human neu
12	307	89.8	57	9	ADY28292 Novel Erb
13	300	87.7	53	6	AAE36804 Human neu
14	300	87.7	56	9	ADY28279 Novel Erb
15	298	87.1	56	3	AA36802 Protein #
16	294	86.0	52	2	AAW05183 Neu diffe
17	294	86.0	52	3	AA36792 EGF-like
18	294	86.0	53	8	AD48886 Human her
19	293	85.7	56	3	AA36801 Protein #
20	287	83.9	50	2	AA87457 GGF2bpb5
21	287	83.9	56	3	AA36811 Protein #
22	282	82.5	56	3	AA36796 Protein #
23	279	81.6	56	3	AA36808 Protein #
24	276	80.7	56	3	AA36799 Protein #

25	276	80.7	56	3	AA36797 Protein #
26	274	80.1	49	5	AA66044 Rat NRG-1
27	274	80.1	52	3	AA36728 EGF-like
28	272	79.5	56	3	AA36804 Protein #
29	272	79.5	56	3	AA36795 Protein #
30	271	79.2	56	3	AA36800 Protein #
31	270	78.9	56	3	AA36798 Protein #
32	269	78.7	56	3	AA36794 Protein #
33	268.5	78.5	49	3	AA36714 EGF-like
34	267	78.1	56	3	AA36805 Protein #
35	266	77.8	52	3	AA36725 EGF-like
36	264.5	77.3	49	3	AA36716 EGF-like
37	263	76.9	52	2	AAW05182 Neu diffe
38	263	76.9	52	3	AA56983 NDF/heres
39	263	76.9	52	3	AA12602 Human NDF
40	263	76.9	56	3	AA36812 Protein #
41	260	76.0	52	2	AAW05185 Neu diffe
42	260	76.0	56	3	AA36809 Protein #
43	256	74.9	56	3	AA36810 Protein #
44	254	74.3	52	3	AA36722 EGF-like
45	252	73.7	56	3	AA36806 Protein #

ALIGNMENTS

RESULT 1
AD45192
ID AD45192 standard; protein; 61 AA.
XX
AC AD45192;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human neuregulin protein SEQ ID NO:4.
XX
KW neuregulin; viral myocarditis; cardiomyopathy; myocardial infarction;
KW cardiac; human.
XX
OS Homo sapiens.
XX
PN WO2003099300-A1.
XX
PD 04-DEC-2003.
XX
PF 15-MAY-2003; 2003WO-CN000355.
XX
PR 24-MAY-2002; 2002WO-CN000349.
XX
PA (ZENS-) ZENSUN SHANGHAI SCI TECH LTD.
XX
PI Zhou M;
XX
WP: 2004-042705/04.
XX
DR N-PSDB; AD45191.
XX
PT New composition comprising neuregulin (NRG), nucleic acid encoding NRG or
PT an agent that enhances the production and/or function of NRG, and a
PT therapeutic agent, useful for treating or preventing heart diseases, e.g.
PT viral myocarditis.
XX
PS Claim 5; SEQ ID NO 4; 146pp; English.
XX
CC The present invention describes a combination comprising: (a) a
CC neuregulin (NRG) protein, a nucleic acid encoding NRG protein and/or function
CC functional fragment, or an agent that enhances production and/or function
CC of NRG; and (b) a prophylactic or therapeutic agent for viral
CC myocarditis, dilated (congestive) cardiomyopathy (DCM), or myocardial
CC infarction. Also described: (1) a method for preventing, treating or
CC infarction viral myocarditis, DCM, cardiac toxicity or myocardial
CC infarction in a mammal by administering a NRG protein, a nucleic acid
CC encoding the protein, their functional fragment, or an agent that
CC enhances production and/or function of NRG; (2) a pharmaceutical

CC composition for preventing, treating or delaying viral myocarditis or DCM
 CC in a mammal comprising a NRG protein, a nucleic acid encoding a NRG
 CC protein, their functional fragment, or an agent that enhances production
 CC and/or function of NRG; (3) a kit comprising the combination above or the
 CC composition in a container, and an instruction for using the combination
 CC in preventing, treating or delaying viral myocarditis, DCM or myocardial
 CC infarction; and (4) a pharmaceutical composition for preventing, treating
 CC or delaying a disease in a mammal comprising a safety dosage equal to or
 CC less than about 170 U/kg, or in a total regimen equal to or less than
 CC about 3600 U/kg. The combination has cardiact activity. The combination
 CC is useful for preventing, treating or delaying viral myocarditis, DCM,
 CC cardiac toxicity or myocardial infarction. NRG can be used to repair
 CC damaged myocardial cell structure, strengthen connection between these
 CC cells, improve myocardial function and strengthen myocardial biological
 CC effect. The present sequence represents a human neuregulin amino acid
 CC sequence which is used in the exemplification of the present invention.
 CC N.B. The present sequence is designated as SEQ ID NO:2 in the Sequence
 CC Listing, but is given as SEQ ID NO:4 on page 36 of the specification, and
 CC is claimed as SEQ ID NO:4.

XX
 SQ Sequence 61 AA;

Query Match 100.0%; Score 342; DB 8; Length 61;
 Best Local Similarity 100.0%; Pred. No. 3.4e-26;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLVKCAEKERTFCVNGGECFVWVDLSNPSRYLCKCNEFTGDRCONVWASFYKARELY 60
 DB 1 SHLVKCAEKERTFCVNGGECFVWVDLSNPSRYLCKCNEFTGDRCONVWASFYKARELY 60

QY 61 Q 61
 DB 61 Q 61

RESULT 2

ADP09196 standard; protein; 61 AA.

AC ADP09196;

DT 26-FEB-2004 (first entry)

XX Human neuregulin beta2 fragment #SEQ ID 1.

XX Cardiant; gene therapy; human; neuregulin; viral myocarditis;

XX dilated cardiomyopathy; DCM.

OS Homo sapiens.

PN WO2003099320-A1.

XX 04-DEC-2003.

PF 24-MAY-2002; 2002WO-CN000349.

PR 24-MAY-2002; 2002WO-CN000349.

XX (ZENS-) ZENSUN SHANGHAI SCI TECH LTD.

PI Zhou M.

DR WPI; 2004-035046/03.

DR N-PSDB; ADP09197.

XX New composition for treating viral myocarditis or dilated cardiomyopathy,

PT comprises a neuregulin protein or nucleic acid, an agent that enhances

PT the production or function of neuregulin, and a prophylactic or

PT therapeutic agent.

PS Claim 5; Page 22; 44pp; English.

XX The invention relates to a composition comprising an amount of a

CC neuregulin protein or its fragment, or a nucleic acid encoding a
 CC neuregulin protein or its fragment, or an agent that enhances production
 CC and/or function of the neuregulin, and an amount of a prophylactic or
 CC therapeutic agent for viral myocarditis or dilated (congestive)
 CC cardiomyopathy (DCM). Also disclosed is a method of preventing, treating
 CC or delaying viral myocarditis or DCM in a mammal. The neuregulin in the
 CC combination carries out its anti-viral myocarditis or anti-DCM activity
 CC via binding with ErbB3-ErbB4 receptors. The prophylactic or therapeutic
 CC agent for viral myocarditis is selected from an antibiotic, a heart
 CC protective agent, an antioxidant and a nutrient for myocardium. The
 CC composition and method of the invention are useful in preventing,
 CC treating or delaying viral myocarditis or dilated cardiomyopathy in
 CC humans. The current sequence represents the amino acid sequence of human
 CC neuregulin beta2 fragment.

XX
 SQ Sequence 61 AA;

Query Match 100.0%; Score 342; DB 8; Length 61;
 Best Local Similarity 100.0%; Pred. No. 3.4e-26;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLVKCAEKERTFCVNGGECFVWVDLSNPSRYLCKCNEFTGDRCONVWASFYKARELY 60
 DB 1 SHLVKCAEKERTFCVNGGECFVWVDLSNPSRYLCKCNEFTGDRCONVWASFYKARELY 60

QY 61 Q 61
 DB 61 Q 61

RESULT 3

ADP32008 standard; protein; 61 AA.

AC ADP32008;

DT 26-FEB-2004 (first entry)

XX Recombinant plasmid from endonuclease digestion.

XX cardiac toxicity; prophylactic; neuregulin protein; Antiarrhythmic;

XX tumor.

OS Unidentified.

PN WO2003099321-A1.

XX 04-DEC-2003.

PF 18-SEP-2002; 2002WO-CN000664.

PR 24-MAY-2002; 2002WO-CN000349.

XX (ZENS-) ZENSUN SHANGHAI SCI TECH LTD.

PI Zhou M.

DR WPI; 2004-042707/04.

DR N-PSDB; ADP32007.

XX Preventing, treating or delaying cardiac toxicity (e.g. arrhythmia) in

PT humans having malignant tumors comprises administering a neuregulin

PT protein, a nucleic acid encoding neuregulin or an agent enhancing

PT function of neuregulin.

PS Claim 22; SEQ ID NO 2; 36pp; English.

XX The present invention relates to preventing, treating or delaying cardiac

CC toxicity in a mammal comprising administering in vivo prophylactic or

CC therapeutic agent and neuregulin protein or its functional fragment,

CC nucleic acid encoding protein, or agent enhancing production or function

CC of neuregulin, where cardiac toxicity associated with administration of

CC prophylactic or therapeutic agent is prevented, treated or delayed. The


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DE EGFL3.
XX
XX Glial growth factor; GGF, heregulin; mitogenesis; Schwann cell; tumour;
KM central nervous system; erbB2 receptor; antiproliferative;
KM epidermal growth factor; EGF.
XX
XX Unidentified.
XX
XX WO9403644-A1.
XX
XX 17-FEB-1994.
XX
XX 10-AUG-1993; 93WO-US007491.
XX
XX
PR 10-AUG-1992; 92US-00927337.
PR 25-SEP-1992; 92US-00951747.
PR 01-DEC-1992; 92US-00984085.
PR 29-JAN-1993; 93US-00011396.
XX
XX (CAMP-) CAMBRIDGE NEUROSCIENCE INC.
XX
XX Gwynne DI, Marchionni M, Mcburney RN;
PI WPI; 1994-065731/08.
XX
XX N-PSDB; AAQ58325.
XX
XX Glial growth factor DNA encoding numerous polypeptide factors used for
PT inhibiting cell proliferation - for treating carcinoma and nervous
PT disorders.
XX
XX Disclosure; Fig 41; 178pp; English.
XX
XX The GGF coding segments include regions with EGF-like homology. These EGF
CC -like domains can be required for the activation of mitogenesis in the
CC binding reaction between GGF ligands contg. such domains and the erbB2
CC receptor. Pref. antiproliferative factors are those which lack these EGF-
CC like domains. (Updated on 10-MAR-2003 to add missing OS field.) (Updated
CC on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 60 AA:
SQ
Query Match 98.5%; Score 337; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SHLVKAEKERTFCVNGGECFMYKDLNPSRYLCKCPNEFTGDRCONYVMAFPYKARELY 60
1 SHLVKAEKERTFCVNGGECFMYKDLNPSRYLCKCPNEFTGDRCONYVMAFPYKARELY 60
DB
RESULT 7
AAR67251
ID AAR67251 standard; protein; 60 AA.
XX
XX AAR67251;
AC
XX 25-MAR-2003 (revised)
DT 15-AUG-1995 (first entry)
XX
XX Human epidermal like growth factor 3 (EGFL3).
XX
XX Epidermal like growth factor 3; mammalian muscle cell treatment; EGFL3.
KM skeletal; cardiac; smooth; acetylcholine receptor deficiency; EGFL3.
XX
XX Homo sapiens.
OS
XX WO9426298-A1.
XX
XX 24-NOV-1994.
XX
XX 06-MAY-1994; 94WO-US005083.
XX
XX 06-MAY-1993; 93US-00059022.
XX

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PR 08-MAR-1994; 94US-00209204.
XX
XX (CAMP-) CAMBRIDGE NEUROSCIENCE.
XX
XX Sklar R, Marchionni M, Gwynne DI;
PI WPI; 1995-006353/01.
XX
XX DR N-PSDB; AAQ74916.
XX
XX Treating mammalian muscle diseases and disorders - by admin. of GGF2 and
PT other specified polypeptide(s) which bind the p185erbB2 receptor.
XX
XX Claim 35; Page 149; 241pp; English.
XX
XX AAQ74916 encodes AAR67251 human epidermal like growth factor 3 (EGFL3).
CC The glial cell mitogenic activity of EGFL3 can be used to treat a variety
CC of mammalian skeletal, cardiac and smooth muscle diseases, including
CC acetylcholine receptor deficiency. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX Sequence 60 AA:
SQ
Query Match 98.5%; Score 337; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SHLVKAEKERTFCVNGGECFMYKDLNPSRYLCKCPNEFTGDRCONYVMAFPYKARELY 60
1 SHLVKAEKERTFCVNGGECFMYKDLNPSRYLCKCPNEFTGDRCONYVMAFPYKARELY 60
DB
RESULT 8
AAR96077
ID AAR96077 standard; peptide; 60 AA.
XX
XX AAR96077;
AC
XX 27-AUG-1996 (first entry)
DT
XX
XX Epidermal growth factor-like domain GGF peptide EGFL3.
XX
XX Glial growth factor; GGF; human; hGGF2; Schwann cell; mitogenesis; GGF-I;
KM glial cell; therapy; neurogulin; heregulin; cellular communication; hEGF;
KM vertebrate; neuron; muscle cell; nervous system; neurotrophic agent;
KM matrix molecule; protease; protease inhibitor; neurological disorder;
KM peripheral neuropathy; amyotrophic lateral sclerosis; nerve injury;
KM spinal muscular atrophy; Alzheimer's disease; spinal cord injury;
KM epidermal growth factor.
XX
XX Synthetic.
OS
XX WO9615812-A1.
XX
XX 30-MAY-1996.
XX
XX 16-NOV-1995; 95WO-US014974.
XX
XX 17-NOV-1994; 94US-00341018.
XX
XX (CAMP-) CAMBRIDGE NEUROSCIENCE INC.
XX
XX Gwynne DI, Mahanthappa NK, Marchionni MA, Bermingham-McDonogh O;
PI Goldin SM, Mcburney RN;
XX
XX WPI; 1996-268341/27.
XX
XX N-PSDB; AAT30991.
XX
XX Use of neurogulin to affect cellular communication in a vertebrate - by
PT admin. of a neurogulin or neurogulin DNA, used to treat neurological
PT disorders, e.g. Alzheimer's disease, peripheral neuropathy etc.
XX
XX Disclosure; Fig 20; 111pp; English.
XX

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CC AAR6075-R6980 represent glial growth factor (GGF) peptides which
 CC encompass the epidermal growth factor-like domain (EGFL). The DNA
 CC encoding these sequences can be used in the method of the invention. This
 CC method is to affect cellular communication in a vertebrate by
 CC administration of neuroregulin or a neuroregulin-producing cell, where the
 CC neuroregulin interacts with a first cell type to form product A, which in
 CC turn affects a function of a second cell type. The effect on the second
 CC cell type results in the production of product B which affects the first
 CC (or a third) cell type. Alternatively a neuroregulin coding sequence is
 CC incorporated into the genome of a vertebrate cell, and the neuroregulin is
 CC then expressed by the cell. The first cell type is a nervous system
 CC support cell, preferably a Schwann cell, neuron or muscle cell. The
 CC second and third cell types are nervous system or muscle cells. Products
 CC A and B are neurotrophic agents, matrix molecules, proteases or protease
 CC inhibitors. The method can be used to treat neurological disorders, such
 CC as peripheral neuropathy, amyotrophic lateral sclerosis, spinal muscular
 CC atrophy, nerve injury, Alzheimer's disease or spinal cord injury. It can
 CC also induce muscle mitogenesis. This method preferably induces more than
 CC one neurotrophic product, and is more effective than using a single
 CC neurotrophic factor, which would tend to have a restricted effect on a
 CC specific neuronal subtype

XX SQ Sequence 60 AA;

Query Match 98.5%; Score 337; DB 2; Length 60;
 Best Local Similarity 100.0%; Pred. No. 1e-25;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLVKAEKERTFCVNGGECFPMVDLSNPSRYLCKPNEFTGDRCONVMAFYKAEELY 60
 1 SHLVKAEKERTFCVNGGECFPMVDLSNPSRYLCKPNEFTGDRCONVMAFYKAEELY 60
 Db 1 SHLVKAEKERTFCVNGGECFPMVDLSNPSRYLCKPNEFTGDRCONVMAFYKAEELY 60

RESULT 9
 AAM09364
 ID AAM09364 standard; protein; 60 AA.
 XX
 AC AAM09364;
 DT 27-AUG-2003 (revised)
 DT 01-JUN-1997 (first entry)
 XX
 DE EGFL3.
 KW Neuroregulin; EGFL3; glial growth factor; GGF; heregulin;
 KW acetylcholine receptor inducing activity; ARIA;
 KW neu differentiation factor; erbB receptor; mitogen; eye; retina;
 KW retinopathy; retinitis pigmentosa; macular degeneration; wound repair.
 XX
 OS Undefined.
 XX
 PN WO9630403-A1.
 PD 03-OCT-1996.
 XX
 PF 27-MAR-1996; 96WO-US004240.
 XX
 PR 27-MAR-1995; 95US-00411295.
 XX
 PA (CAMP-) CAMBRIDGE NEUROSCIENCE INC.
 PI Reh TA, Marchionni MA, McCabe KL, Birmingham-McDonogh O,
 PI Mahanthappa NK, Gwynne DJ;
 XX
 DR WPI; 1996-455276/45.
 DR N-PSDB; AAT48083.
 XX
 PT Use of neuroregulin polypeptide(s) - for the treatment of retinal cells,
 PT partic. for treating retinal diseases or retinal degeneration.
 XX
 PS Claim 32; Fig 20; 102pp; English.
 CC DNA sequences (AAT48081-86) respectively code for EGFL1, EGFL2, EGFL3.

CC EGFL4, EGFL5 and EGFL6 (AAM09362-67) that bind with the erbB receptors of
 CC retinal cells. These polypeptides are useful in new therapeutic
 CC approaches to injury or diseases of the eye, esp. degenerative diseases
 CC of the retina, based on the promotion of retinal cell function. (Updated
 CC on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 60 AA;

Query Match 98.5%; Score 337; DB 2; Length 60;
 Best Local Similarity 100.0%; Pred. No. 1e-25;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLVKAEKERTFCVNGGECFPMVDLSNPSRYLCKPNEFTGDRCONVMAFYKAEELY 60
 1 SHLVKAEKERTFCVNGGECFPMVDLSNPSRYLCKPNEFTGDRCONVMAFYKAEELY 60
 Db 1 SHLVKAEKERTFCVNGGECFPMVDLSNPSRYLCKPNEFTGDRCONVMAFYKAEELY 60

RESULT 10
 AAR87462
 ID AAR87462 standard; protein; 60 AA.
 XX
 AC AAR87462;
 DT 05-JUL-1996 (first entry)
 DT
 XX
 DB Epidermal growth factor-like domain GGF peptide EGFL3.
 XX
 KW Glial growth factor; GGF; human; hGGR2; Schwann cell; mitogenesis; GGF-I;
 KW glial cell; therapy; peripheral nerve damage; demyelination; bovine;
 KW neurodegenerative disorder; neural regeneration; acetylcholine receptor;
 KW fibroblast proliferation; wound repair; multiple sclerosis; glial tumour;
 KW GGF-II epidermal growth factor; hEGF.
 XX
 OS Synthetic.
 XX
 PN WO9532724-A1.
 PD 07-DEC-1995.
 XX
 PF 25-MAY-1995; 95WO-US006846.
 XX
 PR 26-MAY-1994; 94US-00249322.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (CAMP-) CAMBRIDGE NEUROSCIENCE.
 XX
 PI Goodearl AD, Stroobant P, Minghetti L, Waterfield M, Marchionni M;
 PI Chen MS, Hiles I;
 XX
 DR WPI; 1996-030329/03.
 DR N-PSDB; AAT06735.
 XX
 PT Glial growth factors with Schwann cell mitogenic activity - for
 PT prophylaxis or treatment of nerve disorders, e.g. Multiple Sclerosis.
 XX
 PS Example 11; Fig 40; 199pp; English.
 XX
 CC AAR87460-R87465 represent glial growth factor (GGF) peptides which
 CC encompass the epidermal growth factor-like domain (EGFL). These sequences
 CC have Schwann cell mitogenic activity in the presence of foetal calf
 CC plasma. The peptide sequences, and hGGR2 are used to stimulate
 CC mitogenesis of glial cells, for prophylaxis or treatment of a
 CC pathophysiological condition of the nervous system in a mammal. Also, for
 CC identification of a receptor, for treatment of conditions of peripheral
 CC nerve damage (e.g. demyelination/damage/loss of Schwann cells), treatment
 CC of neurodegenerative disorders in mammals, for inducing neural
 CC regeneration, fibroblast proliferation or wound repair. Glial tumours can
 CC be treated by inhibiting this sequence binding to its receptor. These
 CC peptides are also able to induce synthesis of acetylcholine receptor, and
 CC is useful in prophylaxis or treatment of multiple sclerosis in a patient

XX SQ Sequence 60 AA;

Query Match 98.5%; Score 337; DB 2; Length 60;
 Best Local Similarity 100.0%; Pred. No. 1e-25;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLVKAEKREKTCVNGGECFVWKDLSNPSRYLCKCPNEFTGDRCONVYMASFYKAEELY 60
 |||||
 DB 1 SHLVKAEKREKTCVNGGECFVWKDLSNPSRYLCKCPNEFTGDRCONVYMASFYKAEELY 60

RESULT 11

AAB12601
 ID AAB12601 standard; peptide; 58 AA.

XX AAB12601;

XX 09-NOV-2000 (first entry)

DE Human neuregulin beta 2 isoform fragment peptide sequence SEQ ID NO:2.

XX Human; neuregulin; neuregulin beta 2 isoform; epithelial growth factor;

KW EGF; cardiac muscle; cardiomyocyte; growth; differentiation; NRG;

XX heart disease; cardiac; cardioprotective.

XX Homo sapiens.

XX MO200037095-A1.

XX 29-JUN-2000.

XX 21-DEC-1999; 99MO-AU001137.

XX 21-DEC-1998; 98AU-00007850.

XX (CHAN-) CHANG CARDIAC RES INST VICTOR.

XX Zhou M;

XX WPI; 2000-442531/38.

XX N-PSDB; AAA60997.

XX Treating heart disease or heart failure comprises administering

XX neuregulin to enhance cardiomyocyte growth and/or differentiation.

XX Disclosure; Page 11; 44pp; English.

XX The present invention describes a method for inducing cardiomyocyte

XX growth and/or differentiation comprising exposing the cell to neuregulin

XX (NRG) with subsequent activation of the MAP kinase pathway. Neuregulin

XX increases cardiac muscle cell differentiation and organization of

XX sarcomeric and cytoskeletal structures and also enhances cell-to-cell

XX adhesion. The method is useful in the treatment or management of heart

XX disease or failure in a mammal. The present sequence represents a human

XX neuregulin beta 2 isoform peptide fragment, containing the epithelial

XX growth factor (EGF) like domain and the receptor binding domain

XX Sequence 58 AA;

XX Query Match 92.4%; Score 316; DB 3; Length 58;

XX Best Local Similarity 96.7%; Pred. No. 1.1e-23;

XX Matches 58; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 SHLVKAEKREKTCVNGGECFVWKDLSNPSRYLCKCPNEFTGDRCONVYMASFYKAEELY 60
 |||||
 DB 1 SHLVKCA--EKTFCVNGGECFVWKDLSNPSRYLCKCPNEFTGDRCONVYMASFYKAEELY 58

RESULT 12

ADY28292 standard; protein; 57 AA.

XX ADY28292;

XX 05-MAY-2005 (first entry)

XX Novel ErbB ligand-related EGF domain protein region SeqID15.

KW ErbB ligand; EGF domain; neuroprotective; cytoskeletal; vasotropic;

KW vulnery; antiangiogenic; neuroleptic; gene therapy; ErbB receptor;

KW hyperproliferation; neurological disease; psychiatric disorder;

XX angiogenesis disorder; restenosis; wound healing; neurological disease.

XX Homo sapiens.

XX WO2005017096-A2.

XX 24-FEB-2005.

XX 19-AUG-2004; 2004WO-IL000759.

XX 19-AUG-2003; 2003US-0495898P.

XX (AGOS-) AGOS BIOTECH LTD.

XX Harari D;

XX WPI; 2005-173275/18.

XX New polypeptide comprising a splice variant of an ErbB ligand encoded by

XX differential exon usage comprising a truncated EGF domain devoid of the C

XX -loop of the EGF domain, useful in preparing a composition for treating

XX e.g., restenosis.

XX Example; SEQ ID NO 15; 158pp; English.

XX This invention relates to a novel polypeptide which comprises a splice

XX variant of an ErbB ligand encoded by differential exon usage comprising a

XX truncated EGF domain devoid of the C-loop of the EGF domain. The

XX invention may be useful for the development of compounds with a

XX neuroprotective, cytoskeletal, vasotropic, vulnery, antiangiogenic or

XX neuroleptic activity whilst the disclosed sequences may prove useful for

XX gene therapy. The polypeptide is useful in preparing a composition for

XX treating a disease or disorder related to an ErbB receptor or to

XX pathological activity of at least one ErbB receptor. For example

XX neoplastic, hyperproliferative, neurological or psychiatric disorders,

XX angiogenesis, restenosis, wound or neurological injuries. The present

XX sequence is that of an EGF domain protein region which was used during

XX the illustration of the novel polypeptides of the invention.

XX Sequence 57 AA;

XX Query Match 89.8%; Score 307; DB 9; Length 57;

XX Best Local Similarity 100.0%; Pred. No. 8.4e-23;

XX Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLVKAEKREKTCVNGGECFVWKDLSNPSRYLCKCPNEFTGDRCONVYMASFY 54
 |||||
 DB 4 SHLVKAEKREKTCVNGGECFVWKDLSNPSRYLCKCPNEFTGDRCONVYMASFY 57

RESULT 13

AAE36804 standard; protein; 53 AA.

XX AAE36804;

XX 07-AUG-2003 (first entry)

DE Human neuregulin 1 beta EGF-like domain.

XX Epidermal growth factor receptor; EGFR; therapy; psoriasis; carcinoma;

KW cancer; rhabdomyosarcoma; mesothelioma; melanoma; glioblastoma; human;

KW receptor; EGF; neuregulin 1 beta.

XX Homo sapiens.

XX WO2003014159-A1.

```
XX 20-FEB-2003.
PD
XX
XX 05-AUG-2002; 2002WO-AU001042.
PF
XX
XX 03-AUG-2001; 2001AU-00006827.
PR
XX 03-AUG-2001; 2001AU-00006828.
PR 01-NOV-2001; 2001US-0335393P.
PR 01-NOV-2001; 2001US-0336560P.
PR 31-MAY-2002; 2002AU-00002731.
PR 11-JUN-2002; 2002US-0388171P.
XX
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
PA (BIOM-) BIOMOLECULAR RES INST LTD.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PA (LUDW-) LUDWIG INST CANCER RES.
XX
XX Adams TE, Burgess AW, Ellemann TC, Garrett RPJ, Jorissen RN;
PI Lou M, Lovrecz GO, McKern NM, Nice EC, Ward CW;
XX
XX WPI; 2003-268181/26.
DR
XX
XX Selecting or designing compounds that interact with or inhibit formation
PT of active dimers of the EGF receptor family, and useful for the
PT prevention and treatment of disorders, such as psoriasis and cancer of
PT the breast, brain or colon.
XX
XX Disclosure; Fig 2; 354pp; English.
XX
XX The invention relates to a method of selecting or designing a compound
CC that interacts with or inhibits the formation of active dimers of a
CC receptor of the epidermal growth factor receptor (EGFR) family. The
CC methods and compositions of the invention are useful for the prevention
CC and treatment of disorders associated with signalling by a molecule of
CC the EGFR family such as psoriasis and cancer of the pancreas, breast,
CC brain, colon, prostate, ovary, cervix, lung, head and neck, melanoma,
CC rhabdomyosarcoma, mesothelioma, squamous carcinomas of the skin and
CC glioblastomas. The present sequence is epidermal growth factor (EGF) like
CC domain of human neuroligin 1 beta protein. This sequence is used to
CC illustrate the method of the invention
XX
XX Sequence 53 AA;
SQ
XX
XX Query Match 87.7%; Score 300; DB 6; Length 53;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-22;
XX Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SHLVKCAEKEKTFCVNGGECFPMVDLSNPSRYLCKCPNEFTGDRCONYVMASF 53
DB 1 SHLVKCAEKEKTFCVNGGECFPMVDLSNPSRYLCKCPNEFTGDRCONYVMASF 53
XX
XX
XX RESULT 14
XX ADY28279
XX ID ADY28279 standard; protein: 56 AA.
XX
XX AC ADY28279;
XX
XX 05-MAY-2005 (first entry)
XX
XX Novel ErbB ligand-related EGF domain protein region SegID2.
XX
XX ErbB ligand; EGF domain; neuroprotective; cytosolic; vasotrophic;
XX vulnerability; antiangiogenic; neuroleptic; gene therapy; ErbB receptor;
XX hyperproliferation; neurological disease; psychiatric disorder;
XX angiogenesis disorder; restenosis; wound healing; neurological disease.
XX
XX Homo sapiens.
XX
XX MO2005017096-A2.
XX
XX 24-FEB-2005.
XX
XX
```

```
PF 19-AUG-2004; 2004WO-IL000759.
XX
XX 19-AUG-2003; 2003US-0495898P.
PR
XX
XX (AGOS-) AGOS BIOTECH LTD.
XX
XX Harari D;
XX
XX WPI; 2005-173275/18.
DR
XX
XX New polypeptide comprising a splice variant of an ErbB ligand encoded by
PT differential exon usage comprising a truncated EGF domain devoid of the C
PT -loop of the EGF domain, useful in preparing a composition for treating
PT e.g., restenosis.
XX
XX Disclosure; SEQ ID NO 2; 158pp; English.
XX
XX This invention relates to a novel polypeptide which comprises a splice
CC variant of an ErbB ligand encoded by differential exon usage comprising a
CC truncated EGF domain devoid of the C-loop of the EGF domain. The
CC invention may be useful for the development of compounds with a
CC neuroprotective, cytosolic, vasotrophic, vulnerability, antiangiogenic or
CC neuroleptic activity whilst the disclosed sequences may prove useful for
CC gene therapy. The polypeptide is useful in preparing a composition for
CC treating a disease or disorder related to an ErbB receptor or to
CC pathological activity of at least one ErbB receptor, for example
CC neoplastic, hyperproliferative, neurological or psychiatric disorders,
CC angiogenesis, restenosis, wound or neurological injuries. The present
CC sequence is that of an EGF domain protein region which was used during
CC the illustration of the novel polypeptides of the invention.
XX
XX Sequence 56 AA;
SQ
XX
XX Query Match 87.7%; Score 300; DB 9; Length 56;
XX Best Local Similarity 100.0%; Pred. No. 4e-22;
XX Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SHLVKCAEKEKTFCVNGGECFPMVDLSNPSRYLCKCPNEFTGDRCONYVMASF 53
DB 4 SHLVKCAEKEKTFCVNGGECFPMVDLSNPSRYLCKCPNEFTGDRCONYVMASF 56
XX
XX
XX RESULT 15
XX AAB36802
XX ID AAB36802 standard; protein: 56 AA.
XX
XX AC AAB36802;
XX
XX 16-FEB-2001 (first entry)
XX
XX Protein #9.
XX
XX Heregulin; ErbB receptor; transplantation; cancer;
XX nervous system disease; musculature; epithelium.
XX
XX Homo sapiens.
XX
XX US6136558-A.
XX
XX 24-OCT-2000.
XX
XX 09-FEB-1998; 98US-00020880.
XX
XX 10-FEB-1997; 97US-0037581P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Jones JT, Fairbrother WJ, Ballinger MD, Wells JA, Sliwkowski MX;
XX
XX WPI; 2000-678767/66.
XX
XX New variants of heregulin, useful e.g. for treating cancer, comprises
PT specific amino acid alterations that increase affinity for ErbB
PT
```

```

PT receptors.
XX
PS Disclosure; Col 89-90; 58pp; English.
XX
CC The present invention relates to variants of heregulin that can bind to
CC an ErbB receptor and include a portion of the 175-230 region of native
CC human heregulin-beta1. The variants may be used to promote ex vivo
CC survival, proliferation and differentiation of cells, particularly when
CC intended for transplantation. They may also be used to treat a wide range
CC of cancers and diseases of the nervous system, musculature and epithelium
XX
SQ Sequence 56 AA;

```

```

Query Match      87.1%; Score 298; DB 3; Length 56;
Best Local Similarity 96.3%; Pred. No. 6.3e-22;
Matches 52; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 SHLVKCAEKKEKTCVNGGECFVWYKDLNPSRYLCKCPNEFTGDRCONVWASFY 54
   |||||
Db 3 SHLVKCAEKKEKTCVNGGECFVWYKDLNPSRYLCKCPNEFTGDRCONVWASFY 56

```

Search completed: January 26, 2006, 12:42:11
 Job time : 75 secs

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OM protein - protein search, using sw model

Run on: January 26, 2006, 12:33:27 ; Search time 16 seconds

(without alignments)
366.826 Million cell updates/sec

Title: US-09-980-672-2

Sequence: 1 SHLVKCAKEKTFVCNGSEC.....GDRCONVMASFYAEELVQ 61

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 263416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 16431

Minimum DB seq length: 0
Maximum DB seq length: 61

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	122.5	35.8	57	PC4415	ErbB kinase activa
2	77.5	22.7	53	S17294	epidermal growth f
3	69	20.2	46	JT0747	epiregulin - rat
4	68	19.9	50	A61215	transforming growt
5	68	19.9	50	A48545	epidermal growth f
6	59.5	17.4	43	A48998	proteinkinase inhibi
7	46	12.7	53	JX0309	neurotoxin Tx2 - s
8	43.5	12.7	58	S29214	neurotoxin Tx2 - s
9	43.5	12.7	58	A37039	metallothionein 1
10	43	12.6	56	E31440	ovomucoid 2, third
11	42.5	12.4	49	S29173	D-galactose-bindin
12	42.5	12.4	49	F70221	hypothetical prote
13	42	12.3	56	B31441	ovomucoid, third d
14	41	12.0	56	B61494	metallothionein I
15	40.5	11.8	19	A31252	metallothionein I
16	40.5	11.8	38	P0187	Ig lambda chain -
17	40.5	11.8	46	G53613	plectoxin IX - spi
18	40.5	11.8	48	I38217	proteasin-serine/chr
19	40.5	11.8	49	D70228	hypothetical prote
20	40.5	11.8	55	T10344	hypothetical prote
21	40.5	11.8	59	T08149	metallothionein-li
22	40.5	11.8	60	D97932	hypothetical prote
23	40	11.7	37	A59401	delta-palutyl - Pa
24	40	11.7	56	E31438	ovomucoid, third d
25	40	11.7	56	D31440	ovomucoid 1, third
26	40	11.7	56	F61493	ovomucoid, third d
27	40	11.7	57	T2NJR	short toxin CM-1b
28	40	11.7	58	SKMD18	metallothionein 1
29	40	11.7	61	T13448	hypothetical prote

30	39.5	11.5	37	2	A60963	charybotoxin 1 [v
31	38.5	11.5	49	2	S29215	neurotoxin Tx2 - s
32	39.5	11.5	58	2	S30496	protein kinase Mpk
33	39.5	11.5	55	2	F75180	hypothetical prote
34	39	11.4	20	2	A48394	major fat-globule
35	39	11.4	38	1	C35030	cutarotoxin III - f
36	39	11.4	48	2	S29216	neurotoxin Tx2 - s
37	39	11.4	54	2	A61494	ovomucoid (PSTI-ty
38	39	11.4	54	2	H61493	ovomucoid (PSTI-ty
39	39	11.4	54	2	C31443	ovomucoid, third d
40	39	11.4	56	2	A31445	ovomucoid, third d
41	39	11.4	56	2	H31439	ovomucoid, third d
42	39	11.4	56	2	E31437	ovomucoid, third d
43	39	11.4	56	2	E31442	ovomucoid, third d
44	39	11.4	56	2	I31439	ovomucoid, third d
45	39	11.4	56	2	G61493	ovomucoid (PSTI-ty

ALIGNMENTS

RESULT 1

PC4415

ErbB kinase activator beta, brain and thymus - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 10-Dec-1997 #sequence_revision 10-Dec-1997 #text_change 08-Sep-2002

C/Accession: PC4415

R/Higashiyama, S.; Horikawa, M.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa, T.; Miy.

J. Biochem. 122, 675-680, 1997

A/Title: A novel brain-derived member of the epidermal growth factor family that inter-

A/Reference number: J05700; MUID:98006324; PMID:9348101

A/Accession: PC4415

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-57 <HIG>

A/Cross-references: UNIPARC:UPI00000170767; DDBJ:D89997; NID:g2605633; PIDN:BAA2346.1;

A/Experimental source: PC-12 cell

C/Comment: This protein is a member of the epidermal growth factor family. It is functi

ating the differentiation of MDA-MB-453 cells.

C/Superfamily: human ErbB kinase activator alpha, brain and thymus; EGF homology; immu

F/1-25/Domain: EGF homology (fragment) <EGF>

Query Match 35.8%; Score 122.5; DB 2; Length 57;

Best Local Similarity 50.0%; Pred. No. 2.8e-07;

Matches 22; Conservative 8; Mismatches 11; Indels 3; Gaps 1;

Cy 18 GECFMVMDLSRPSRYLCKPWEFTGDRCONVMASFYAEELVQ 61
Db 1 GVCYYIRGINQLS---CKCPVGYTGDRCONQFAMVNFSAEELVQ 41

RESULT 2

S17294

epidermal growth factor - pig (fragment)

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C/Accession: S17294

R/Pascall, J.C.; Jones, D.S.C.; Doel, S.M.; Clements, J.M.; Hunter, M.; Fallon, T.; Ed

J. Mol. Endocrinol. 6, 63-70, 1991

A/Title: Cloning and characterization of a gene encoding pig epidermal growth factor.

A/Reference number: S17294; MUID:91197366; PMID:2015058

A/Accession: S17294

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-53 <PAS>

A/Cross-references: UNIPROT:Q00968; UNIPARC:UPI000002D1A4; EMBL:X59516; NID:g1940; PIDN

C/Superfamily: epidermal growth factor precursor; EGF homology; LDL receptor ITID-conta

F/6-42/Domain: EGF homology <EGF>

Query Match 22.7%; Score 77.5; DB 2; Length 53;
Best Local Similarity 27.9%; Pred. No. 0.038; Indels 3; Gaps 1;
Matches 12; Conservative 11; Mismatches 17;

RESULT 8

S29214

neurotoxin Tx2 - spider (Phonetreria nigriVenter)

C/Species: Phonetreria nigriVenter

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999

C/Accession: S29214

Rido Nascimento Cordeiro, M.; Ribeiro Diniz, C.; do Carmo Valentim, A.; von Eickstedt, V.

FEBS Lett. 310, 153-156, 1992

A/Title: The purification and amino acid sequences of four Tx2 neurotoxins from the venom of *Phonetreria nigriVenter*

A/Reference number: S29214; PMID:93011905; PMID:1397265

A/Accession: S29214

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-53 <COR>

A/Cross-references: UNIPARC:UPI00001766CD

C/Superfamily: curatoloxin

Query Match 12.7%; Score 43.5; DB 2; Length 53;

Best Local Similarity 30.8%; Pred. No. 3.e+02;

Matches 16; Conservative 6; Mismatches 15; Indels 15; Gaps 3;

QY 6 CAERK-----TFCVNGGECFVMDLSPSRYLCKCPNEFTGDRCONVVA 51

Db 3 CAGQDKCKCKDCGGERGEC--VCAISYEGKRCIC-----RQGNFLIA 45

RESULT 9

A37039

metallothionein 1 - American lobster

C/Species: Homarus americanus (American lobster)

C/Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 09-Jul-2004

C/Accession: A37039

R. Browner, M.; Winge, D.R.; Gray, W.R.

J. Inorg. Biochem. 35, 289-303, 1989

A/Title: Structural and functional diversity of copper-metallothioneins from the American lobster *Homarus americanus*

A/Reference number: A37039; PMID:85215793; PMID:2709004

A/Accession: A37039

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-58 <BRO>

A/Cross-references: UNIPROT:P29499; UNIPARC:UPI0000177C98

C/Superfamily: metallothionein

Query Match 12.7%; Score 43.5; DB 2; Length 58;

Best Local Similarity 29.3%; Pred. No. 3.2e+02;

Matches 12; Conservative 4; Mismatches 4; Indels 21; Gaps 3;

QY 5 KCAEKETFCVNGGECFVMDLSPSRYLCKCPNEFTGDRG 45

Db 26 RCAPCEK--CTSG-----CKCPK--DEC 45

RESULT 10

E31440

ovomucoid 2, third domain - gray junglefowl (fragment)

C/Species: Gallus sonnerati

C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 19-Apr-2002

C/Accession: E31440

R. Labkovski, J.F.; Kato, I.; Ardelt, W.; Cook, J.; Empe, A.; Empe, M.W.; Kohr, W.U.

Biochemistry 26, 202-221, 1987

A/Title: Ovomucoid third domains from 100 avian species: isolation, sequences, and hyper-

A/Reference number: A90515; PMID:87157615; PMID:3828298

A/Accession: E31440

A/Molecule type: protein

A/Residues: 1-56 <LAS>

A/Cross-references: UNIPARC:UPI00001762C7

A/Experimental source: Gallus sonnerati (gray junglefowl)

A/Note: the authors designate this sequence with the code OMCJFV

C/Superfamily: ovomucoid; Kazal proteinase inhibitor homology

C/Keywords: egg white; glycoprotein; serine proteinase inhibitor

F:6-56/Domain: Kazal proteinase inhibitor homology <KPI>

F:8-38,16-35,24-56/Diulfide bonds: #status predicted

F:45/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 12.6%; Score 43; DB 2; Length 56;

Best Local Similarity 31.4%; Pred. No. 3.6e+02;

Matches 16; Conservative 6; Mismatches 15; Indels 14; Gaps 3;

QY 4 VKAEKKTFCVNGGECFVMDLSPSRYLCKCPNEFTGDRGQ--NYMAS 52

Db 6 VDCSEYKPKDCT-----VED-----RPLGSDNKTGKNCNNAVES 44

RESULT 11

S29173

D-galactose-binding lectin II - Axinella polyoides (fragment)

C/Species: Axinella polyoides

C/Date: 19-Mar-1997 #sequence_revision 14-Nov-1997 #text_change 09-Jul-2004

C/Accession: S29173

R. Buck, F.; Luth, C.; Strupat, K.; Bretting, H.

Biochim. Biophys. Acta 1159, 1-8, 1992

A/Title: Comparative investigations on the amino-acid sequences of different isolectins

A/Reference number: S29172; PMID:93003351; PMID:1390906

A/Accession: S29173

A/Molecule type: protein

A/Residues: 1-49 <BUC>

A/Cross-references: UNIPROT:P28587; UNIPARC:UPI000012E3B2.

Query Match 12.4%; Score 42.5; DB 2; Length 49;

Best Local Similarity 37.0%; Pred. No. 3.6e+02;

Matches 10; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 6 CAEKETFCVNGGECFVMDLSPSRYLCKCPNEFTGDRG 32

Db 4 CAERQK-YIVONLETALYLVNPSGY 29

RESULT 12

F70221

hypothetical protein BBD02 / BBH03 - Lyme disease spirochete plasmids lp17 and lp28-3

C/Species: Borrelia burgdorferi (Lyme disease spirochete)

C/Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004

C/Accession: F70221; E70235

R. Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Tachigra, R.; Whit-

son, D.; Peterson, J.; Krelavage, A.R.; Quackenbush, J.; Salberg, S.; Hanson, M.; Vugt

; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A/Authors: Smith, H.O.; Venter, J.C.

A/Title: Genomic sequence of a Lyme disease spirochete, *Borrelia burgdorferi*.

A/Reference number: A70100; PMID:98065943; PMID:9403685

A/Accession: F70221

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-49 <KLE>

A/Cross-references: UNIPROT:O54556; UNIPARC:UPI00000132E; GB:AE000793; NID:G2689927; P

A/Experimental source: strain B31

A/Accession: E70235

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-49 <KLE>

A/Cross-references: UNIPARC:UPI00000132E; GB:AE000784; NID:G2690041; PID:AA65997.1;

A/Experimental source: strain B31

C/Genetics:

A/Genome: plasmid

A/Note: one copy each on linear plasmids lp17 (BBD02) and lp28-3 (BBH03); a close homol-

Query Match 12.4%; Score 42.5; DB 2; Length 49;

Best Local Similarity 33.3%; Pred. No. 3.6e+02;

Matches 15; Conservative 7; Mismatches 16; Indels 7; Gaps 2;

QY 5 KCAEKETFCVNGGECFVMDLSPSRYLCKCPNEFTGDRGQ 49

Db 8 KCSIIEKT-----QLEIINNSIEKQLHQLIEFTG-VCLLYV 45

RESULT 13

B31441

Ovomucoid, third domain - gray francolin (fragment)

C/Species: Francolinus pondicerianus (gray francolin)

C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #ext_change 09-Jul-2004

C/Accession: B31441

R/Laskowski Jr., M.; Kato, I.; Ardelt, W.; Cook, J.; Denton, A.; Empe, M.W.; Kohr, W.J.

Biochemistry 26, 202-221, 1987

A/Title: Ovomucoid third domains from 100 avian species: isolation, sequences, and hyper

A/Reference number: A90515; MUID:87157615; PMID:3828298

A/Accession: B31441

A/Molecule type: protein

A/Residues: 1-56 <IAS>

A/Cross-references: UNIPROT:P05598; UNIPARC:UPI000012D783

A/Note: the authors designate this sequence with the code OMGRF3

C/Superfamily: ovomucoid; Kazal proteinase inhibitor homology

C/Keywords: egg white; glycoprotein; serine proteinase inhibitor

F/6-56/Domain: Kazal proteinase inhibitor homology <KPI>

F/8-38,16-35,24-56/Disulfide bonds: #status predicted

F/45/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

12.3%; Score 42; DB 2; Length 56;

Best Local Similarity 27.5%; Pred. No. 4.6e+02;

Matches 14; Conservative 6; Mismatches 17; Indels 14; Gaps 2;

QY 4 VKCAEKETFCVNGEGCFMWKDLSPRYLCKCPNEFTGDRQ--NYVMAS 52

DB 6 VDCSEYKPPDC-----TTERPLCGSDNKTGKNCNCAVNES 44

RESULT 14

B61494

Ovomucoid (PRTI-type proteinase inhibitor), third domain - Congo peafowl (fragment)

C/Species: Afropavo congenis (Congo peafowl)

C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #ext_change 09-Jul-2004

C/Accession: B61494; B31115

R/Laskowski Jr., M.; Apostol, I.; Ardelt, W.; Cook, J.; Gilletto, A.; Kelly, C.A.; Lu, W.

J. Protein Chem. 9, 715-725, 1990

A/Title: Amino acid sequences of ovomucoid third domain from 25 additional species of b

A/Reference number: A61492; MUID:91158808; PMID:2073323

A/Accession: B61494

A/Molecule type: protein

A/Residues: 1-56 <IAS>

A/Cross-references: UNIPROT:P52258; UNIPARC:UPI000012D75A

C/Superfamily: ovomucoid; Kazal proteinase inhibitor homology

C/Keywords: egg white; glycoprotein; serine proteinase inhibitor

F/6-56/Domain: Kazal proteinase inhibitor homology <KPI>

F/8-38,16-35,24-56/Disulfide bonds: #status predicted

F/45/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

12.0%; Score 41; DB 2; Length 56;

Best Local Similarity 27.5%; Pred. No. 6.1e+02;

Matches 14; Conservative 6; Mismatches 17; Indels 14; Gaps 2;

QY 4 VKCAEKETFCVNGEGCFMWKDLSPRYLCKCPNEFTGDRQ--NYVMAS 52

DB 6 VDCSEYKPPAC-----TMEQRPLCGSDNKTGKNCNCAVNES 44

RESULT 15

A31252

metallothionein I - yeast (Candida glabrata) (fragment)

C/Species: Candida glabrata

C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #ext_change 09-Jul-2004

C/Accession: A31252

R/Mehra, R.K.; Tarbet, E.B.; Gray, W.R.; Winge, D.R.

Proc. Natl. Acad. Sci. U.S.A. 85, 8815-8819, 1988

A/Title: Metal-specific synthesis of two metallothioneins and gamma-glutamyl peptides in

A/Reference number: A94212; MUID:89057829; PMID:3194392

A/Accession: A31252

A/Molecule type: protein

A/Residues: 1-19 <MEH>

A/Cross-references: UNIPROT:P5113; UNIPARC:UPI0000177CA5

C/Superfamily: metallothionein

Query Match

11.8%; Score 40.5; DB 2; Length 19;

Best Local Similarity 57.1%; Pred. No. 2.6e+02;

Matches 8; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 34 CKCPNEFTGDRQCN 47

DB 4 CKCPN---GCSPN 14

Search completed: January 26, 2006, 12:43:55
Job time: 17 secs

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OM protein - protein search, using sw model1

Run on: January 26, 2006, 12:31:01 ; Search time 67 seconds
(without alignments)
642.347 Million cell updates/sec

Title: US-09-980-672-2

Perfect score: 342
Sequence: 1 SHLVKCAKEKTEFCVNGSEC.....GDRCONVMAFYKAEELVQ 61

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 129292

Minimum DB seq length: 0
Maximum DB seq length: 61

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	160	46.8	58	2	086WJ0 HUMAN
2	141.5	41.4	54	2	0810X1 MOUSE
3	74	21.6	42	2	08WY1 HUMAN
4	70.5	20.6	53	2	06QBS2 HUMAN
5	70	20.5	34	2	068D87 HUMAN
6	70	20.5	36	2	072663 HUMAN
7	68	19.9	50	1	TGFA_RABIT
8	68	19.9	50	2	Q7M0A9 MESAU
9	66	19.3	50	2	Q6QBS1 HUMAN
10	61.5	18.0	59	2	Q4T175 TETNG
11	59	17.3	57	2	Q5IEC4 HUMAN
12	58.5	17.1	44	2	Q4S1D4 TETNG
13	55	16.1	39	2	Q9MZ77 BOVIN
14	55	16.1	61	2	Q84KT0 BRAOL
15	53.5	15.6	52	2	Q9TX97 CAEL
16	51	14.9	37	2	Q5VVG4 HUMAN
17	50	14.6	57	2	Q64QMS BACFR
18	49.5	14.5	36	2	Q4T2A0 TETNG
19	49.5	14.5	42	1	SEK1_CENGR
20	48.5	14.2	37	2	Q6L8Y4 HUMAN
21	46.5	13.6	51	2	Q9CQH4 MOUSE
22	46.5	13.6	55	2	Q5TC39 HUMAN
23	46	13.5	57	2	Q95S09 DROME
24	46	13.5	61	1	IBB_BRVVA
25	45	13.2	34	2	Q8F634 LEPIN
26	45	13.2	39	2	O18628 SCHMA
27	45	13.2	34	2	Q7Y500 BPR69
28	45	13.2	56	2	Q4XQW9 PLACH
29	45	13.2	58	2	Q69BD0 CAMJE
30	45	13.2	58	2	Q69B10 CAMCO
31	45	13.2	60	2	Q4ZU96_PSEBY

32	45	13.2	60	2	0883A4 PSESM
33	44.5	13.0	42	1	SEK1_CENEL
34	44.5	13.0	47	2	Q934J1 CARPI
35	44.5	13.0	48	2	Q55AE1 dictyostell
36	44.5	12.9	37	2	Q86B27 9CAEN
37	44	12.9	54	1	TX36_PHOKE
38	44	12.9	56	2	Q4HDT4 CAMCO
39	44	12.9	59	2	Q5YAS2_9CAUD
40	44	12.9	60	2	Q4KE11_PSEFS
41	43.5	12.7	58	1	MT1_HOMAM
42	43.5	12.7	58	2	Q5P38 HOMAM
43	43	12.6	40	2	Q5M419 STRT2
44	43	12.6	47	2	Q91X04_9ENNO
45	43	12.6	51	2	Q8DT16_STRMU

ALIGNMENTS

RESULT 1					
ID	086WJ0 HUMAN	PRELIMINARY;	PRT;	58 AA.	
AC	086WJ0;				
DT	01-JUN-2003 (TREMBLrel. 24, Created)				
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)				
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DE	Neuregulin 1 isoform 4 (Fragment).				
GN	Name=NRG1;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;				
OC	Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RX	MDLINE=22993650; PubMed=14632199;				
RX	DOI=10.1046/j.1523-1747.2003.12522.x;				
RA	Stove C.P., Stove V., Derycke U., Van Marck V., Mareel M., Bracke M.;				
RT	"The heregulin/human epidermal growth factor receptor as a new growth factor system in melanoma with multiple ways of deregulation.";				
RL	J. Invest. Dermatol. 121:802-812(2003).				
RN	[2]				
RP	NUCLEOTIDE SEQUENCE.				
RA	Stove C.P., Stove V., Mareel M., Bracke M.;				
RL	Submitted (DEC-2002) to the EMBL/Genbank/DBJ databases.				
DR	EMBL; AY207002; AAC9724.1; -; mRNA.				
DR	HSSP; Q12780; 1HAE.				
DR	SMR; 086WJ0: 1-47.				
DR	InterPro; IPR000742; EGF_2.				
DR	InterPro; IPR006209; EGF_1like.				
DR	InterPro; IPR006210; IEGF.				
DR	Pfam; PF00008; EGF_1.				
DR	SMART; SM00181; EGF_1.				
DR	PROSITE; PS00022; EGF_1; 1.				
DR	PROSITE; PS01186; EGF_2; 1.				
DR	PROSITE; PS50026; EGF_3; 1.				
KW	EGF-like domain.				
FT	NON TER				
SQ	SEQUENCE 58 AA; 6299 MW; 48F31PCE4E5A1FB CRC64;				
Query Match					
Best Local Similarity 80.6%; Score 160; DB 2; Length 58;					
Matches 29; Conservative 0; Mismatches 7; Indels 0; Gaps 0;					
Oy	14	CVNGGECFMYVDLSNPSRYLCKCPNFTGRCCQYV	49		
Db	1	CVNGGECFMYVDLSNPSRYLCKCPNFTGRCCQYV	36		
RESULT 2					
ID	0810X1 MOUSE				
AC	0810X1; MOUSE PRELIMINARY;		PRT;	54 AA.	

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DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Neuregulin 2-beta (Fragment).
GN Name=Nrg2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CD-1; TISSUE=Olfactory bulb;
RX PubMed=15039062; DOI=10.1016/j.pep.2003.12.012;
RA Mautino B., Dalla Costa L., Gambardella G., Petroleanu I., Fasolo A.,
RA Dati C.;
RT "Bioactive recombinant neuregulin-1, -2, and -3 expressed in
RT Escherichia coli."
RL Protein Expr. Purif. 35:25-31(2004).
DR EMBL; AY227026; AAC072523.1; -; mRNA.
DR HSSP; P01133; 1JL9.
DR MGI; MGI:1098246; Nrg2.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00008; EGF_1.
DR SMART; SM00181; EGF_1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
KW EGF-like domain.
FT NON_TER 1 54
FT NON_TER 54 54
SQ SEQUENCE 54 AA; 6019 MW; C25NA17AD0BA59A CRC64;

Query Match 41.4%; Score 141.5; DB 2; Length 54;
Best Local Similarity 47.1%; Pred. No. 2.6e-09;
Matches 24; Conservative 10; Mismatches 14; Indels 3; Gaps 1;

OY 5 KCAEKEKTCVNGGECFMVNDLSNPSRYLCKPNEFTGDRCONVMAFYK 55
DB 1 KCNETAKSYCVNGGVCYIRGINLS---CKCPGYTGDRCCQPRAMNPFK 48

RESULT 3
08MWY1 HUMAN
ID 08MWY1_HUMAN PRELIMINARY; PRT; 42 AA.
AC 08MWY1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE CBH1 isoform III (Crumbs homolog 1) (Drosophila) (Fragment).
GN Name=CRB1; ORFNames=RP11-53124.1-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99438399; PubMed=10508521; DOI=10.1038/13848;
RA den Hollander A.I., ten Brink J.B., de Kok Y.J.M., van Soest S.,
RA van den Born L.I., van Driel M.A., van de Pol D.J.R., Payne A.M.,
RA Bhatnagar S.S., Kellner U., Hoyng C.B., Westerveld A.,
RA Brunner H.G., Bleeker-Wagemakers E.M., Deutman A.F.,
RA Heckenlively J.R., Cremers F.P.M., Bergen A.A.B.;
RT "Mutations in a human homologue of Drosophila crumbs cause retinitis
RT pigmentosa (RP12).";
RL Nat. Genet. 23:217-221(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21592405; PubMed=11734541; DOI=10.1093/hmg/10.24.2767;
RA den Hollander A.I., Johnson K., de Kok Y.J.M., Klebes A.,

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RA Brunner H.G., Knust E., Cremers F.P.M.;
RT "CRB1 has a cytoplasmic domain that is functionally conserved between
RT human and Drosophila.";
RL Hum. Mol. Genet. 10:2767-2773(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Smith M.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Holt K.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY043323; AAL10680.1; -; mRNA.
DR EMBL; AL136322; CA116645.1; -; Genomic_DNA.
DR EMBL; AL139136; CA115310.1; -; Genomic_DNA.
DR EMBL; AL139136; CA116645.1; JOINED; Genomic_DNA.
DR EMBL; AL136322; CA115310.1; JOINED; Genomic_DNA.
DR HSSP; P08709; 1BF9.
DR Ensemble; ENSG00000134376; Homo sapiens.
DR GO; GO:0005509; F-actin ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR00742; EGF_2.
DR InterPro; IPR001881; EGF_Ca_bd.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00008; EGF_1.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00179; EGF_CA; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
KW EGF-like domain.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 42 AA; 4630 MW; 407D112FAF090D15 CRC64;

Query Match 21.6%; Score 74; DB 2; Length 42;
Best Local Similarity 40.5%; Pred. No. 0.25;
Matches 17; Conservative 6; Mismatches 11; Indels 8; Gaps 3;

OY 5 KCAEKEKTCVNGGECFMVNDLSNPSRYLCKPNEFTGDRCCQ 46
DB 6 ECASDP---CVNGGLC---QDLIN--KFCGLCVAFAGEKCE 39

RESULT 4
06QBS2 HUMAN
ID 06QBS2_HUMAN PRELIMINARY; PRT; 53 AA.
AC 06QBS2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Epidermal growth factor (Fragment).
GN Name=EGF;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nguyen N.L., Do Q.H., Vu M.T., Nguyen B.N., Phan V.C.;
RT "Cloning of a gene encoding for a human epidermal growth factor.";
RL Y Hoc Viet Nam 298:43-45(2004).
DR EMBL; AY548762; AAS83395.1; -; mRNA.
DR HSSP; P01132; 1A3P.
DR SMR; 06QBS2; 3-50.
DR InterPro; IPR001336; EGF_1.
DR InterPro; IPR00742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00008; EGF_1.
DR PRINTS; PR00009; EGFTR.

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DR SMART; SM00181; EGF; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
DR EGF-like domain; Growth factor.
FT NON_TER 1 1
FT NON_TER 53 53
SQ SEQUENCE 53 AA; 6222 MW; 7D6A806D873B071 CRC64;

Query Match
Best Local Similarity 20.6%; Score 70.5; DB 2; Length 53;
Matches 12; Conservative 9; Mismatches 18; Indels 3; Gaps 1;

Qy 5 KCAEKETFCVNGGECFVMDLSPRYLCKCPHEFTGDRQ 46
Db 5 ECLPSHDGCLHDGVCVYIEAL--DKYACNCVGVYIGRCQ 43

RESULT 5
Q68D87_HUMAN PRELIMINARY; PRT; 34 AA.
AC Q68D87;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein DKFZp79N0541 (Fragment).
GN Name=DKFZp79N0541;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo
NCBI_Taxid=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RG The German cDNA Consortium;
RA Koehler K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Podo G., Han M., Wiemann S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR749519; CAH18333.1; -; mRNA.
KM Hypothetical protein.
FT NON_TER 34 34
SQ SEQUENCE 34 AA; 3678 MW; 1FB19C9A9FC42240 CRC64;

Query Match
Best Local Similarity 20.5%; Score 70; DB 2; Length 34;
Matches 10; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Qy 2 HLKCAEKETFCVNGGECFVMDLSP 29
Db 5 HEBPCGSHKSFCLNGCLGVIPPIPS 32

RESULT 6
Q72663_HUMAN PRELIMINARY; PRT; 36 AA.
AC Q72663;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZp79N1944.
GN Name=DKFZp79N1944;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo
NCBI_Taxid=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Bloecher H., Bloecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Podo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

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DR EMBL; BX538100; CAD98015.1; -; mRNA.
KM Hypothetical protein.
SQ SEQUENCE 36 AA; 3963 MW; 56287FB19C9A9FC4 CRC64;

Query Match
Best Local Similarity 20.5%; Score 70; DB 2; Length 36;
Matches 10; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Qy 2 HLKCAEKETFCVNGGECFVMDLSP 29
Db 5 HEBPCGSHKSFCLNGCLGVIPPIPS 32

RESULT 7
TGFA_RABIT STANDARD; PRT; 50 AA.
ID TGFA_RABIT
AC P98138;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Transforming growth factor alpha (TGF-alpha) (EGF-like TGF) (ETGF)
DE (TGF type 1) (Fragment).
GN Name=TGFA;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
NCBI_Taxid=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93150169; PubMed=8426908; DOI=10.1016/0167-0115(93)90405-W;
RA Goldring J.R., Tsunoda Y., Stoch S.A., Coffey R.J., Modlin I.M.;
RT "Transforming growth factor-alpha (TGF alpha) inhibition of parietal
cell secretion: structural requirements for activity.";
RL Regul. Pept. 43:37-47(1993).
CC -1- FUNCTION: Inhibitor of acid secretion. Inhibitor of aminopyrine
uptake in parietal cells (in vitro).
CC -1- SUBUNIT: Interacts with the PDZ domains of SDCBP and SNTAL. The
interaction with SDCBP is required for the targeting to the cell
surface (By similarity).
CC -1- TISSUE SPECIFICITY: Gastric parietal cells.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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DR EMBL; M86827; AAA73200.1; -; mRNA.
DR PIR; A48545; A48545.
DR HSSP; P01135; 3TGF.
DR SMR; P98138; 2-50.
DR InterPro; IPR001336; EGF_1.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00008; EGF_1.
DR PRINTS; PR00009; EGF_TGF.
DR SMART; SM00181; EGF_1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
KM EGF-like domain; Growth factor; Mitogen.
FT DOMAIN 4 44 EGF-like.
FT DISULFID 8 21 By similarity.
FT DISULFID 16 32 By similarity.
FT DISULFID 34 43 By similarity.
FT NON_TER 1 1
FT NON_TER 50 50
SQ SEQUENCE 50 AA; 5565 MW; BDD508F4053625DB CRC64;

Query Match
Best Local Similarity 19.9%; Score 68; DB 1; Length 50;

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Best Local Similarity 27.7%; Pred. No. 1.5;
Matches 13; Conservative 11; Mismatches 19; Indels 4; Gaps 1;

OY 1 SHLVKAEKEKTEPCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCON 47
DB 3 SHFNCPSDHTQPCFHGTCTFLVOE----DKPACVCHSGYVGARCEH 45

RESULT 8

Q7M0A9_MESAU PRELIMINARY; PRT; 50 AA.
ID Q7M0A9; AC Q7M0A9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Transforming growth factor alpha precursor (Fragment).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Cricetinae; Mesocricetus.
NCBI_TaxID=10036;

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9183613; PubMed=2009597;
RA Chiang T., McBride J., Chou M.Y., Nishimura I., Wong D.T.W.;
RT "Molecular cloning of the complementary DNA encoding for the hamster
TGF-alpha mature peptide.";
RL Carcinogenesis 12:529-532(1991).
DR PIR; A61215; A61215.
DR HSSP; P01135; IMOX.
DR SMR; Q7M0A9; 2-50.

DR InterPro; IPR001336; EGF_1.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00008; EGF_1.
DR PRINTS; PR00009; EGF_TGF.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
KW Growth factor.

FT NON_TER 1 1
FT 50 50
SQ SEQUENCE 50 AA; 5580 MW; FCD508B454732000 CRC64;

Query Match 19.9%; Score 68; DB 2; Length 50;
Best Local Similarity 27.7%; Pred. No. 1.5;
Matches 13; Conservative 11; Mismatches 19; Indels 4; Gaps 1;

OY 1 SHLVKAEKEKTEPCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCON 47
DB 3 SHFNCPSDHTQPCFHGTCTFLVOE----DKPACVCHSGYVGARCEH 45

RESULT 9

Q6QBS1_HUMAN PRELIMINARY; PRT; 50 AA.
ID Q6QBS1; AC Q6QBS1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transforming growth factor alpha (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;

RP NUCLEOTIDE SEQUENCE.
RA Phan V.C., Nguyen B.N., Do Q.H.;
RT "Molecular cloning and sequence analysis of the transforming growth
factor alpha gene from Homo sapiens placenta.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY548763; AAS83396.1; -, mRNA.

DR SMR; Q6QBS1; 2-50.
DR InterPro; IPR001336; EGF_1.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00008; EGF_1.
DR PRINTS; PR00009; EGF_TGF.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
KW Growth factor.

FT NON_TER 1 1
FT 50 50
SQ SEQUENCE 50 AA; 5552 MW; BDD508E5053634DB CRC64;

Query Match 19.3%; Score 66; DB 2; Length 50;
Best Local Similarity 27.7%; Pred. No. 2.7;
Matches 13; Conservative 10; Mismatches 20; Indels 4; Gaps 1;

OY 1 SHLVKAEKEKTEPCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCON 47
DB 3 SHFNCPSDHTQPCFHGTCTFLVOE----DKPACVCHSGYVGARCEH 45

RESULT 10

Q4T175_TETNG PRELIMINARY; PRT; 59 AA.
ID Q4T175; AC Q4T175;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF2358, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00000101001;
OS Tetradon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
NCBI_TaxID=99883;

RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Coataz C., Bernot A.,
RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Caselli V., Katinka M., Vacherie B.,
RA Blemond C., Skali Z., Cattolico L., Poulain J., De Bernardis V.,
RA Cruaud C., Duprat S., Broctier P., Coutureau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kelis M., Wolff JN., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lauder V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetradon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
[2]

RP NUCLEOTIDE SEQUENCE.
RG Genoscope, Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; CA601002358; CA67407.1; -, Genomic DNA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca_bd.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00008; EGF_1.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00179; EGF_CA; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.

DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS50026; EGF_3; 2.
 KW EGF-like domain.
 FT NON_TER 59
 SQ SEQUENCE 59 AA; 6207 MW; 6BD9E51E9C47F351 CRC64;
 Query Match 18.0%; Score 61.5; DB 2; Length 59;
 Best Local Similarity 37.5%; Pred. No. 11;
 Matches 12; Conservative 3; Mismatches 12; Indels 5; Gaps 1;
 Oy 14 CVNGGECFVMDLSPSRYLCKPNEFTGDRCC 45
 Db 4 CANGATC-----LQGVNRFSCVCPFGSGRRC 30

RESULT 11
 OS IEBC4_HUMAN
 ID OSIEC4_HUMAN PRELIMINARY; PRT; 57 AA.
 AC OSIEC4; 57-SEP-2005 (TREMBlrel. 30, Created)
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
 DE Netrin G1 isoform G11 (Fragment).
 GN Name=NTNG1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RA Meerbach J.M.A., Ohba H., Fukasawa M., Aoki M., Yoshikawa T.;
 RT "Human netrin G1 isoforms show evidence of differential expression.";
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY764264; AA047411.1; -, mRNA.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR006209; EGF_1like.
 DR InterPro; IPR006210; IEGF.
 DR SMART; SM00181; EGF; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS50026; EGF_3; 1.
 FT NON_TER 1
 FT NON_TER 57
 SQ SEQUENCE 57 AA; 5983 MW; 74C6F2B66FB8475E CRC64;
 Query Match 17.3%; Score 59; DB 2; Length 57;
 Best Local Similarity 30.8%; Pred. No. 21;
 Matches 12; Conservative 4; Mismatches 15; Indels 8; Gaps 1;
 Oy 8 EKEKTFVNGGECFVMDLSPSRYLCKPNEFTGDRCC 46
 Db 14 DNELLHCNGGTC-----NNVRCICPAAYTIGLCE 44

RESULT 12
 OS IJ4_TETNG
 ID OSIJ4_TETNG PRELIMINARY; PRT; 44 AA.
 AC OSIJ4; 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Chromosome 5 SCAF14581, whole genome shotgun sequence.
 GN (Fragment).
 GN ORNames=GSTENG00017665001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
 OC Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OC NCBI_TaxID=998683;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costez C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anhouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cartolico L., Poulain J., De Bernardis V.,
 RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Guzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.U., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Landier V., Schachter V., Querier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissenbach J., Roest Croliels H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope, Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CA00104581; CAP99538.1; -, Genomic_DNA.
 DR InterPro; IPR000152; Axx_hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001481; EGF_Ca_bd.
 DR InterPro; IPR001438; EGF_11.
 DR InterPro; IPR006209; EGF_1like.
 DR InterPro; IPR006210; IEGF.
 DR Pfam; PF00008; EGF; 1.
 DR PRINTS; PR00010; EGFBL00D.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00179; EGF_Ca; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50026; EGF_3; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 KW EGF-like domain.
 FT NON_TER 1
 FT NON_TER 44
 SQ SEQUENCE 44 AA; 4609 MW; 5A1DB8F7089FAC67 CRC64;
 Query Match 17.1%; Score 58.5; DB 2; Length 44;
 Best Local Similarity 30.3%; Pred. No. 19;
 Matches 10; Conservative 7; Mismatches 11; Indels 5; Gaps 1;
 Oy 14 CVNGGECFVMDLSPSRYLCKPNEFTGDRCC 46
 Db 10 CLNGGTC-----VDEVNQFSCVCSKSGSGPCCQ 37

RESULT 13
 OS MZF7_BOVIN
 ID OSMZ7_BOVIN PRELIMINARY; PRT; 39 AA.
 AC OSMZ7; 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Tissue plasminogen activator (Fragment).
 GN Name=PLAT;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20380829; PubMed=10920240; DOI=10.1007/s003350010130;
 RA Sonstegard T.S., Garrett W.M., Ashwell M.S., Bennett G.L.,
 RA Kappes S.M., Van Tassel C.P.;
 RT "Comparative map alignment of BTA27 and HSA4 and 8 to identify

RT Conserved segments of genome containing fat deposition QTL."

RL Mamm. Genome 11:682-688(2000). Genomic_DNA.
 DR EMBL; AF230195; AAF79125.1; -;
 DR HSSP; P00750; ITPG.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR000001; Kringle.
 DR Pfam; PF00051; Kringle; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50026; EGF_3; 1.
 DR Kringle.
 KM
 FT NON_TER 1 1
 FT 39 39
 SQ SEQUENCE 39 AA; 4236 MW; BDB3A28B38A67ECB CRC64;

Query Match 16.1%; Score 55; DB 2; Length 39;
 Best Local Similarity 37.5%; Pred. No. 43;
 Matches 9; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 32 YLCKCPNEFTGDRCONVMA5FYK 55
 Db 2 FVCCPEGFMGKLCIEDATATCYK 25

RESULT 14

Q84KT0_BRAOL PRELIMINARY; PRT; 61 AA.
 ID Q84KT0_BRAOL PRELIMINARY;
 AC Q84KT0;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE S-locus protein 11 (Fragment).
 GN Names=SP11-64;
 OS Brassica oleracea (Cauliflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Brassica.
 OC NCBI_TaxID=3712;
 OX NCBI_TaxID=3712;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=2286392; PubMed=12399400;
 RA Sato K., Nishio T., Kimura R., Kusaba M., Suzuki T., Hatakeyama K.,
 RT Oekendon D.T., Satra Y.;
 RT "Coevolution of the S-locus genes SRK, SLG and SP11/SCR in Brassica
 oleracea and B. rapa."
 RL Genetics 162:931-940(2002).
 DR EMBL; AB054751; BAC24085.1; -; mRNA.
 DR InterPro; IPR006209; EGF_like.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR NON_TER 1 1
 FT 61 AA; 6749 MW; 0744977FB9C07B34 CRC64;
 SQ SEQUENCE 61 AA; 6749 MW; 0744977FB9C07B34 CRC64;

Query Match 16.1%; Score 55; DB 2; Length 61;
 Best Local Similarity 50.0%; Pred. No. 67;
 Matches 11; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

QY 29 PSRYLCKPNEFTGDRCONVYM 50
 Db 41 PSK--CKCSNBSDGRGCVLYI 60

RESULT 15

Q9TX97_CAEEL PRELIMINARY; PRT; 52 AA.
 ID Q9TX97_CAEEL PRELIMINARY;
 AC Q9TX97;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE GLP-1 protein (Fragment).
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=93091267; PubMed=1457827;
 RA Kodoyianni V., Maine E.M., Kimble J.;
 RT "Molecular basis of loss-of-function mutations in the glp-1 gene of
 Caenorhabditis elegans."
 RL Mol. Biol. Cell 3:1199-1213(1992).
 DR InterPro; IPR006209; EGF_like.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR NON_TER 1 1
 FT 52 AA; 5782 MW; E56E1F31B64A0859 CRC64;
 SQ SEQUENCE 52 AA; 5782 MW; E56E1F31B64A0859 CRC64;

Query Match 15.6%; Score 53.5; DB 2; Length 52;
 Best Local Similarity 26.8%; Pred. No. 87;
 Matches 11; Conservative 6; Mismatches 15; Indels 9; Gaps 2;

QY 6 CAEKEKTCVNGGECFMTVDLSNPSRYLCKCPNEFTGDRQ 46
 Db 21 CSRSNGTY-YNDRCTII-----NGFCVCEPDYIGDRCE 52

Search completed: January 26, 2006, 12:43:29
 Job time : 69 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 26, 2006, 12:40:22 ; Search time 23 Seconds
(without alignments)
219.270 Million cell updates/sec

Title: US-09-980-672-2

Perfect score: 342
Sequence: 1 SHLVKAEKKEKTCVNGGEC.....GDRCONVMAFYKAEELY 61

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 323677

Minimum DB seq length: 0
Maximum DB seq length: 61

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/1/1aa/5/COMB.pep: *
2: /cgn2_6/prodata/1/1aa/6/COMB.pep: *
3: /cgn2_6/prodata/1/1aa/H_COMB.pep: *
4: /cgn2_6/prodata/1/1aa/PC/US_COMB.pep: *
5: /cgn2_6/prodata/1/1aa/RE_COMB.pep: *
6: /cgn2_6/prodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	337	98.5	60	2	US-08-341-018-64
2	337	98.5	60	2	US-08-470-335-222
3	337	98.5	60	2	US-08-470-339-222
4	337	98.5	60	2	US-08-467-602-416
5	337	98.5	60	2	US-08-411-295F-99
6	337	98.5	60	2	US-08-411-295F-99
7	298	87.1	56	2	US-09-020-880-102
8	298	87.1	56	2	US-09-101-544-102
9	294	86.0	52	1	US-08-417-640A-2
10	294	86.0	52	1	US-08-760-815-2
11	294	86.0	52	1	US-08-761-038-2
12	294	86.0	52	2	US-09-020-880-92
13	294	86.0	52	2	US-09-101-544-92
14	294	86.0	53	2	US-09-097-681-18
15	294	86.0	54	1	US-08-179-481-112
16	293	85.7	56	2	US-09-020-880-101
17	293	85.7	56	2	US-09-101-544-101
18	287	83.9	50	1	US-08-036-555B-151
19	287	83.9	50	1	US-08-469-569-151
20	287	83.9	50	1	US-08-249-322A-151
21	287	83.9	50	1	US-08-469-526A-151
22	287	83.9	50	1	US-08-734-591A-151
23	287	83.9	50	1	US-08-469-660-151
24	287	83.9	50	2	US-08-470-335-151
25	287	83.9	50	2	US-08-735-021-151
26	287	83.9	50	2	US-08-735-021-190
27	287	83.9	50	2	US-08-734-664A-151

28	287	83.9	50	2	US-08-470-339-151	Sequence 151, App
29	287	83.9	50	2	US-08-467-602-151	Sequence 151, App
30	287	83.9	50	4	PCT-US94-05083C-147	Sequence 147, App
31	287	83.9	50	4	PCT-US95-06846A-151	Sequence 151, App
32	287	83.9	56	2	US-09-020-880-111	Sequence 111, App
33	287	83.9	56	2	US-09-101-544-111	Sequence 111, App
34	286	83.6	50	2	US-08-753-007A-14	Sequence 14, App
35	286	83.6	50	2	US-09-398-496-14	Sequence 14, App
36	282	82.5	56	2	US-09-020-880-96	Sequence 96, App
37	282	82.5	56	2	US-09-101-544-96	Sequence 96, App
38	279	81.6	56	2	US-09-020-880-108	Sequence 108, App
39	279	81.6	56	2	US-09-101-544-108	Sequence 108, App
40	277	81.0	48	2	US-08-899-437-15	Sequence 15, App
41	277	81.0	48	2	US-09-126-121-15	Sequence 15, App
42	276	80.7	56	2	US-09-020-880-97	Sequence 97, App
43	276	80.7	56	2	US-09-020-880-97	Sequence 97, App
44	276	80.7	56	2	US-09-101-544-97	Sequence 97, App
45	276	80.7	56	2	US-09-101-544-99	Sequence 99, App

ALIGNMENTS

```
RESULT 1
US-08-341-018-64
; Sequence 64, Application US/08341018A
; Patent No. 6087323
; GENERAL INFORMATION:
; APPLICANT: Gwynne, David I.
; APPLICANT: Mahanthappa, Nagesh K.
; APPLICANT: Marchionni, Mark A.
; APPLICANT: Birmingham-McDonogh, Olivia
; APPLICANT: McBurney, Robert N.
; TITLE OF INVENTION: USE OF NEUREGULINS AS MODULATORS OF
; FILE REFERENCE: 04585/041001
; CURRENT APPLICATION NUMBER: US/08/341,018A
; CURRENT FILING DATE: 1994-11-17
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-341-018-64

Query Match      98.5%: Score 337; DB 2; Length 60;
Best Local Similarity 100.0%: Pred. No. 9.1e-33;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 SHLVKAEKKEKTCVNGGECFWMYDLSNPSRYLCKCFNEFTGDRCONVMAFYKAEELY 60
Db      1 SHLVKAEKKEKTCVNGGECFWMYDLSNPSRYLCKCFNEFTGDRCONVMAFYKAEELY 60

RESULT 2
US-08-470-335-222
; Sequence 222, Application US/08470335F
; Patent No. 6147190
; GENERAL INFORMATION:
; APPLICANT: GOODERL, ANDREW
; APPLICANT: STROOBANT, PAUL
; APPLICANT: MINGHERTTI, LOUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; FILE REFERENCE: 04585/00200B
; CURRENT APPLICATION NUMBER: US/08/470,335F
; CURRENT FILING DATE: 1995-06-06
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? EARLIER APPLICATION NUMBER: 08/036,555
? EARLIER FILING DATE: 1993-03-24
? NUMBER OF SEQ ID NOS: 252
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO: 222
? LENGTH: 60
? TYPE: PRT
? ORGANISM: Homo sapiens
? OS=08-470-335-222

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Query Match	98.5%	Score 337	DB 2	Length 60
Best Local Similarity	100.0%	Pred. No. 9.1e-33		
Matches 60	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy 1 SHLVKAEKEKTFVNGGECFMWKDLSNBSRYLCKCPNETGTGRQNYMASFYKAEELY 60

Db 1 SHLVKAEKEKTFVNGGECFMWKDLSNBSRYLCKCPNETGTGRQNYMASFYKAEELY 60

RESULT 3
US-08-470-339-222
; Sequence 222, Application US/08470339C

```

; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROBETT, PAUL
; APPLICANT: MINCHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 04585/002008
; CURRENT APPLICATION NUMBER: US/08/470,339C
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; EARLIER APPLICATION NUMBER: 07/940,389
; EARLIER FILING DATE: 1992-09-03
; EARLIER APPLICATION NUMBER: 07/907,138
; EARLIER FILING DATE: 1992-06-30
; EARLIER APPLICATION NUMBER: 07/863,703
; EARLIER FILING DATE: 1992-04-03
; EARLIER APPLICATION NUMBER: 91 07566.3 GB
; EARLIER FILING DATE: 1999-04-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 222
; LENGTH: 60
; TYPE: PRN
; ORGANISM: Homo sapiens
; US-08-470-339-222

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Query Match 98.5%; Score 337; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 9.1e-33;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 SHLVKCAEKEKTPCVNGGECFMVYDLSNPSRYLCKCPNEFTGDRCONYVMAFYKAEELY 600

Db 1 SHLVKCAEKEKTPCVNGGECFMVYDLSNPSRYLCKCPNEFTGDRCONYVMAFYKAEELY 600

RESULT 4
US-08-467-602-416
; Sequence 416, Application US/08467602C

```

; GENERAL INFORMATION:
; APPLICANT: Sklar, Robert
; APPLICANT: Marchionni, Mark
; APPLICANT: Gwynne, David I.
; TITLE OF INVENTION: METHODS FOR TREATING MUSCLE DISEASES AND
; TITLE OF INVENTION: DISORDERS

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? FILE REFERENCE: 04585,028003
? CURRENT APPLICATION NUMBER: US/08/467,602Q
? CURRENT FILING DATE: 1995-06-06
? EARLIER APPLICATION NUMBER: 08/209,204
? EARLIER FILING DATE: 1994-03-08
? EARLIER APPLICATION NUMBER: 08/059,022
? EARLIER FILING DATE: 1993-05-06
? NUMBER OF SEQ ID NOS: 420
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO: 416
? LENGTH: 60
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-08-467-602-416

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Query Match	98.5%	Score 337	DB 2	Length 60
Best Local Similarity	100.0%	Pred. No. 9.1e-33		
Matches 60; Conservative	0	Mismatches 0	Indels 0	Gaps 0

Qy 1 SHLYCAEKETFCVNGGCECFVWKDLSNPSRYLCKPNEFTGDRCONYMASFYKAEELY 600

Db 1 SHLYCAEKETFCVNGGCECFVWKDLSNPSRYLCKPNEFTGDRCONYMASFYKAEELY 600

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RESULT 5
US-08-411-295F-57
; Sequence 57, Application US/08411295F
; Patent No. 6750196
; GENERAL INFORMATION:
; APPLICANT: REH, THOMAS A.
; APPLICANT: MARCHIONNI, MARK A.
; APPLICANT: MCCABE, KATHYRN L.
; APPLICANT: BIRMINGHAM-MCDONOUGH, OLIVIA
; APPLICANT: MAHANTHAPPA, NAGESH K.
; APPLICANT: GWYNNE, DAVID I.
; TITLE OF INVENTION: Methods of Treating Disorders of the Eye
; FILE REFERENCE: 04585/039001
; CURRENT APPLICATION NUMBER: US/08/411,295F
; CURRENT FILING DATE: 1995-03-27
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 60
; TYPE: prt
; ORGANISM: Homo sapiens
US-08-411-295F-57

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Query Match	98.5%	Score 337	DB 2	Length 60
Best Local Similarity	100.0%	Pred. No. 9.1e-33		
Matches 60	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy 1 SHLVKAEKETFCVNGGCECFWVKDLSNPSRYLCKCPNEFTGDRQNYWASFYKAEELY 600

Db 1 SHLVKAEKETFCVNGGCECFWVKDLSNPSRYLCKCPNEFTGDRQNYWASFYKAEELY 600

RESULT 6
US-08-411-295F-99

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: Sequence 99, Application US/08411295F
: Patent No. 6750196
:
: GENERAL INFORMATION:
:
: APPLICANT: REH, THOMAS A.
: APPLICANT: MARCHIONNI, MARK A.
: APPLICANT: MCCABE, KATHYRN L.
: APPLICANT: BERMINGHAM-MCDONOUGH, OLIVIA
: APPLICANT: MAHANTHAPRA, NAGESH K.
: APPLICANT: GWYNNE, DAVID I.
: TITLE OF INVENTION: Methods of Treating Disorders of the Eye
: FILE REFERENCE: 04585/039001
: CURRENT APPLICATION NUMBER: US/08/411,295F
: CURRENT FILING DATE: 1995-03-27
: NUMBER OF SEQ ID NOS: 329
: SOFTWARE: FastSeq for Windows Version 4.0

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SEQ ID NO 99
 LENGTH: 60
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-08-411-295F-99

Query Match 98.5%; Score 337; DB 2; Length 60;
 Best Local Similarity 100.0%; Pred. No. 9.1e-33;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLVKAEKKEKTCFVNGGECFMVVDLSNPSRYLCKCPNEFTGDRCONVMA5FY 60
 DB 1 SHLVKAEKKEKTCFVNGGECFMVVDLSNPSRYLCKCPNEFTGDRCONVMA5FYAEELY 60

RESULT 7
 US-09-020-880-102
 Sequence 102, Application US/09020880A
 Patent No. 6136558
 GENERAL INFORMATION:
 APPLICANT: Genentech, Inc.
 APPLICANT: Ballinger, Marcus D.
 APPLICANT: Jones, Jennifer T.
 APPLICANT: Fairbrother, Wayne J.
 APPLICANT: Sliwowski, Mark X.
 APPLICANT: Wells, James A.
 TITLE OF INVENTION: HERGULIN VARIANTS
 FILE REFERENCE: 14918-720CON1
 CURRENT APPLICATION NUMBER: US/09/020, 880A
 CURRENT FILING DATE: 1998-02-09
 EARLIER APPLICATION NUMBER: US 60/037,581
 EARLIER FILING DATE: 1997-02-10
 NUMBER OF SEQ ID NOS: 116
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 102
 LENGTH: 56
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-020-880-102

Query Match 87.1%; Score 298; DB 2; Length 56;
 Best Local Similarity 96.3%; Pred. No. 3.4e-28;
 Matches 52; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLVKAEKKEKTCFVNGGECFMVVDLSNPSRYLCKCPNEFTGDRCONVMA5FY 54
 DB 3 SHLVKAEKKEKTCFVNGGECFMVVDLSNPSRYLCKCPNEFTGDRCONVMA5FY 56

RESULT 8
 US-09-101-544-102
 Sequence 102, Application US/09101544
 Patent No. 6387638
 GENERAL INFORMATION:
 APPLICANT: Genentech, Inc.
 APPLICANT: Ballinger, Marcus D.
 APPLICANT: Jones, Jennifer T.
 APPLICANT: Fairbrother, Wayne J.
 APPLICANT: Sliwowski, Mark X.
 APPLICANT: Wells, James A.
 TITLE OF INVENTION: HERGULIN VARIANTS
 FILE REFERENCE: 14918-720CON2
 CURRENT APPLICATION NUMBER: US/09/101,544
 CURRENT FILING DATE: 1998-07-17
 PRIOR APPLICATION NUMBER: US 09/020,880
 PRIOR FILING DATE: 1998-02-09
 PRIOR APPLICATION NUMBER: US 60/037,581
 PRIOR FILING DATE: 1997-02-10
 NUMBER OF SEQ ID NOS: 116
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 102
 LENGTH: 56
 TYPE: PRT

ORGANISM: Homo sapiens
 US-09-101-544-102

Query Match 87.1%; Score 298; DB 2; Length 56;
 Best Local Similarity 96.3%; Pred. No. 3.4e-28;
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLVKAEKKEKTCFVNGGECFMVVDLSNPSRYLCKCPNEFTGDRCONVMA5FY 54
 DB 3 SHLVKAEKKEKTCFVNGGECFMVVDLSNPSRYLCKCPNEFTGDRCONVMA5FY 56

RESULT 9
 US-08-417-640A-2
 Sequence 2, Application US/08417640A
 Patent No. 5670342
 GENERAL INFORMATION:
 APPLICANT: Carnahan, Josette F.
 APPLICANT: Hara, Shinichi
 APPLICANT: Lu, Hsieng S.
 APPLICANT: Mayer, John P.
 APPLICANT: Yoshinaga, Steven K.
 TITLE OF INVENTION: NDF Peptides
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Amgen Inc.
 STREET: 1840 Denavilland Drive
 CITY: Thousand Oaks
 STATE: California
 COUNTRY: USA
 ZIP: 91320
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/417,640A
 FILING DATE:
 CLASSIFICATION: 436
 ATTORNEY/AGENT INFORMATION:
 NAME: Mazza, Richard J.
 REFERENCE/DOCKET NUMBER: A-310
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 52 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-417-640A-2

Query Match 86.0%; Score 294; DB 1; Length 52;
 Best Local Similarity 100.0%; Pred. No. 9.3e-28;
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLVKAEKKEKTCFVNGGECFMVVDLSNPSRYLCKCPNEFTGDRCONVMA5 52
 DB 1 SHLVKAEKKEKTCFVNGGECFMVVDLSNPSRYLCKCPNEFTGDRCONVMA5 52

RESULT 10
 US-08-760-815-2
 Sequence 2, Application US/08760815
 Patent No. 5686415
 GENERAL INFORMATION:
 APPLICANT: Carnahan, Josette F.
 APPLICANT: Hara, Shinichi
 APPLICANT: Lu, Hsieng S.
 APPLICANT: Mayer, John P.
 APPLICANT: Yoshinaga, Steven K.
 TITLE OF INVENTION: NDF Peptides
 NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,815
; FILING DATE: 05-DEC-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/417,640
; FILING DATE: 06-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mazza, Richard J.
; REFERENCE/DOCKET NUMBER: A-310
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-760-815-2

Query Match 86.0%; Score 294; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 9.3e-28;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SHLVKCAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONVYMAS 52
Db 1 SHLVKCAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONVYMAS 52

RESULT 11
; US-08-761-038-2
; Sequence 2, Application US/08761038
; Patent No. 5929032
; GENERAL INFORMATION:
; APPLICANT: Carnahan, Josette F.
; APPLICANT: Hara, Shinichi
; APPLICANT: Lu, Hsieng S.
; APPLICANT: Mayer, John P.
; APPLICANT: Yoshinaga, Steven K.
; TITLE OF INVENTION: NDF Peptides
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,038
; FILING DATE: 05-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/417,640
; FILING DATE: 06-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mazza, Richard J.

; REFERENCE/DOCKET NUMBER: A-310
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-761-038-2

Query Match 86.0%; Score 294; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 9.3e-28;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SHLVKCAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONVYMAS 52
Db 1 SHLVKCAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONVYMAS 52

RESULT 12
; US-09-020-880-92
; Sequence 92, Application US/09020880A
; Patent No. 6136558
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ballinger, Marcus D.
; APPLICANT: Jones, Jennifer T.
; APPLICANT: Fairbrother, Wayne J.
; APPLICANT: Sliwkowski, Mark X.
; APPLICANT: Wells, James A.
; TITLE OF INVENTION: HERGULIN VARIANTS
; FILE REFERENCE: 14918-720CON1
; CURRENT APPLICATION NUMBER: US/09/020,880A
; CURRENT FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: US 60/037,581
; EARLIER FILING DATE: 1997-02-10
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 92
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-020-880-92

Query Match 86.0%; Score 294; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 9.3e-28;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SHLVKCAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONVYMAS 52
Db 1 SHLVKCAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONVYMAS 52

RESULT 13
; US-09-101-544-92
; Sequence 92, Application US/09101544
; Patent No. 6387638
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ballinger, Marcus D.
; APPLICANT: Jones, Jennifer T.
; APPLICANT: Fairbrother, Wayne J.
; APPLICANT: Sliwkowski, Mark X.
; APPLICANT: Wells, James A.
; TITLE OF INVENTION: HERGULIN VARIANTS
; FILE REFERENCE: 14918-720CON2
; CURRENT APPLICATION NUMBER: US/09/101,544
; CURRENT FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: US 09/020,880
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/037,581
; PRIOR FILING DATE: 1997-02-10
; NUMBER OF SEQ ID NOS: 116

SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 92
LENGTH: 52
TYPE: PRT
ORGANISM: Homo sapiens
US-09-101-544-92

Query Match 86.0%; Score 294; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 9.3e-28;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SHLVKAEKEKTFVNGGECFVMDLSNPSRYLCKCPNEFTGDRCONVYMAS 52
Db 1 SHLVKAEKEKTFVNGGECFVMDLSNPSRYLCKCPNEFTGDRCONVYMAS 52

RESULT 14

US-09-097-681-18
Sequence 18, Application US/09097681
Patent No. 6727077
GENERAL INFORMATION:
APPLICANT: Young, Paul
APPLICANT: King, C. Richter
APPLICANT: HJazi, Mai
APPLICANT: Ruben, Steve
TITLE OF INVENTION: Heregulin-Like Factor
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/049,942
FILING DATE: 17-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hoover, Kenley K.
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PF383PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8439
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 53 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-097-681-18

Query Match 86.0%; Score 294; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 9.5e-28;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SHLVKAEKEKTFVNGGECFVMDLSNPSRYLCKCPNEFTGDRCONVYMAS 52
Db 2 SHLVKAEKEKTFVNGGECFVMDLSNPSRYLCKCPNEFTGDRCONVYMAS 53

RESULT 15
US-08-179-481-112

Sequence 112, Application US/08179481
Patent No. 5624816
GENERAL INFORMATION:
APPLICANT: CARRAWAY, KERMIT L.
APPLICANT: CAROTHERS, CARRAWAY, CORALIE A.
APPLICANT: FREGIEN, NEVIS L.
TITLE OF INVENTION: ONCOGENE PRODUCT LIGAND
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/179,481
FILING DATE: 28-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/922,521
FILING DATE: 30-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 200702/UM92-08CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-179-481-112

Query Match 86.0%; Score 294; DB 1; Length 54;
Best Local Similarity 100.0%; Pred. No. 9.7e-28;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SHLVKAEKEKTFVNGGECFVMDLSNPSRYLCKCPNEFTGDRCONVYMAS 52
Db 3 SHLVKAEKEKTFVNGGECFVMDLSNPSRYLCKCPNEFTGDRCONVYMAS 54

Search completed: January 26, 2006, 12:44:29
Job time : 23 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 12:43:33 ; Search time 113 Seconds
(without alignments)
225.554 Million cell updates/sec

Title: US-09-980-672-2

Perfect score: 342
Sequence: 1 SHLVKCAEKETFCVNGSEC.....GDRCONYMASFYKAEILYQ 61

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 620404

Minimum DB seq length: 0
Maximum DB seq length: 61

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications AA Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	300	87.7	53	US-10-485-683-13	Sequence 13, Appl
2	298	87.1	56	US-10-082-747A-102	Sequence 102, App
3	294	86.0	52	US-10-082-747A-92	Sequence 92, Appl
4	294	86.0	53	US-10-609-370-18	Sequence 18, Appl
5	293	85.7	56	US-10-082-747A-101	Sequence 101, App
6	287	83.9	50	US-08-736-019-151	Sequence 151, App
7	287	83.9	50	US-10-844-218-151	Sequence 151, App
8	287	83.9	56	US-10-082-747A-111	Sequence 111, App
9	286	83.6	50	US-10-036-241-14	Sequence 14, Appl
10	286	83.6	50	US-10-899-227-14	Sequence 14, Appl
11	282	82.5	56	US-10-082-747A-96	Sequence 96, Appl
12	279	81.6	56	US-10-082-747A-108	Sequence 108, App
13	277	81.0	48	US-09-817-647-15	Sequence 15, Appl
14	277	81.0	48	US-09-877-655-15	Sequence 15, Appl
15	277	81.0	48	US-10-136-573A-15	Sequence 15, Appl
16	277	81.0	48	US-10-215-862-15	Sequence 15, Appl
17	277	81.0	48	US-10-944-116-15	Sequence 15, Appl
18	277	81.0	48	US-11-035-787-15	Sequence 15, Appl
19	276	80.7	56	US-10-082-747A-97	Sequence 97, Appl
20	276	80.7	56	US-10-082-747A-99	Sequence 99, Appl
21	274	80.1	49	US-10-240-411-4	Sequence 4, Appl
22	274	80.1	52	US-10-082-747A-28	Sequence 28, Appl
23	272	79.5	56	US-10-082-747A-95	Sequence 95, Appl
24	272	79.5	56	US-10-082-747A-104	Sequence 104, App
25	271	79.2	56	US-10-082-747A-100	Sequence 100, App
26	270	78.9	56	US-10-082-747A-98	Sequence 98, Appl
27	269	78.7	56	US-10-082-747A-94	Sequence 94, Appl

28	268.5	78.5	49	US-10-082-747A-14	Sequence 14, Appl
29	267	78.1	56	US-10-082-747A-105	Sequence 105, App
30	266	77.8	52	US-10-082-747A-25	Sequence 25, Appl
31	264.5	77.3	49	US-10-082-747A-16	Sequence 16, Appl
32	263	76.9	56	US-10-082-747A-112	Sequence 112, App
33	260	76.0	56	US-10-082-747A-109	Sequence 109, App
34	256	74.9	56	US-10-082-747A-110	Sequence 110, App
35	254	74.3	52	US-10-082-747A-22	Sequence 22, Appl
36	252	73.7	56	US-10-082-747A-106	Sequence 106, App
37	251	73.4	56	US-10-082-747A-103	Sequence 103, App
38	251	73.4	56	US-10-082-747A-115	Sequence 115, App
39	250	73.1	52	US-10-082-747A-29	Sequence 29, Appl
40	248	72.5	56	US-10-082-747A-113	Sequence 113, App
41	244	71.3	50	US-10-036-241-15	Sequence 15, Appl
42	244	71.3	50	US-10-899-227-15	Sequence 15, Appl
43	238	69.6	52	US-10-082-747A-17	Sequence 17, Appl
44	236.5	69.2	49	US-10-082-747A-21	Sequence 21, Appl
45	236	69.0	56	US-10-082-747A-107	Sequence 107, App

ALIGNMENTS

```

RESULT 1
US-10-485-683-13
; Sequence 13, Application US/10485683
; Publication No. US20040248196A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, TIMOTHY EDWARD
; APPLICANT: BURGESS, ANTONY WILKS
; APPLICANT: EILEMAN, THOMAS CHARLES
; APPLICANT: GARRETT, THOMAS PETER JOHN
; APPLICANT: JORISSEN, ROBERT NICHOLAS
; APPLICANT: LOU, MEIZHEN
; APPLICANT: LOVRECEZ, GEORGE OSCAR
; APPLICANT: MCKERN, NEIL MORETON
; APPLICANT: NICE, EDOUARD COLLINS
; APPLICANT: WARD, COLIN WESLEY
; TITLE OF INVENTION: METHODS OF SCREENING BASED ON THE EGF RECEPTOR CRYSTAL
; FILE REFERENCE: 051654/0104
; CURRENT APPLICATION NUMBER: US/10/485,683
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: PCT/AU02/01042
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: AU PR 6827
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: AU PR 6828
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/336,560
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/335,393
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: AU PS 2731
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/388,171
; PRIOR FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-683-13

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Query Match 87.7%; Score 300; DB 5; Length 53;
Best Local Similarity 100.0%; Pred. No. 9.9e-28;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SHLVKCAEKETFCVNGSEC...GDRCONYMASFYKAEILYQ 53
1 SHLVKCAEKETFCVNGSEC...GDRCONYMASFYKAEILYQ 53

RESULT 2
US-10-082-747A-102
; Sequence 102, Application US/10082747A
; Publication No. US20030129688A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ballinger, Marcus D.
; APPLICANT: Jones, Jennifer T.
; APPLICANT: Fairbrother, Wayne J.
; APPLICANT: Sliwkowski, Mark X.
; APPLICANT: Wells, James A.
; TITLE OF INVENTION: HERGULIN VARIANTS
; FILE REFERENCE: 402E-476112US
; CURRENT APPLICATION NUMBER: US/10/082,747A
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/101,544
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: PCT/US/98/01579
; PRIOR FILING DATE: 1998-02-10
; PRIOR APPLICATION NUMBER: US 08/799,054
; PRIOR FILING DATE: 1997-02-10
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 102
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-082-747A-102

Query Match 87.1%; Score 298; DB 4; Length 56;
Best Local Similarity 96.3%; Pred. No. 1.8e-27;
Matches 52; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLVKAEKERTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYMASFY 54
|||
Db 3 SHLVKAEKERTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYMASFY 56

RESULT 3
US-10-082-747A-92
; Sequence 92, Application US/10082747A
; Publication No. US20030129688A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ballinger, Marcus D.
; APPLICANT: Jones, Jennifer T.
; APPLICANT: Fairbrother, Wayne J.
; APPLICANT: Sliwkowski, Mark X.
; APPLICANT: Wells, James A.
; TITLE OF INVENTION: HERGULIN VARIANTS
; FILE REFERENCE: 402E-476112US
; CURRENT APPLICATION NUMBER: US/10/082,747A
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/101,544
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: PCT/US/98/01579
; PRIOR FILING DATE: 1998-02-10
; PRIOR APPLICATION NUMBER: US 08/799,054
; PRIOR FILING DATE: 1997-02-10
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 92
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-082-747A-92

Query Match 86.0%; Score 294; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.9e-27;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLVKAEKERTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYMAS 52

Db 1 SHLVKAEKERTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYMAS 52
|||

RESULT 4
US-10-609-370-18
; Sequence 18, Application US/10609370
; Publication No. US20040048295A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: Heterogulin-Like Factor
; FILE REFERENCE: PF383D1
; CURRENT APPLICATION NUMBER: US/10/609,370
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: 09/097,681
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/049,942
; PRIOR FILING DATE: 1997-06-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-609-370-18

Query Match 86.0%; Score 294; DB 4; Length 53;
Best Local Similarity 100.0%; Pred. No. 5e-27;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLVKAEKERTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYMAS 52
|||
Db 2 SHLVKAEKERTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYMAS 53

RESULT 5
US-10-082-747A-101
; Sequence 101, Application US/10082747A
; Publication No. US20030129688A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ballinger, Marcus D.
; APPLICANT: Jones, Jennifer T.
; APPLICANT: Fairbrother, Wayne J.
; APPLICANT: Sliwkowski, Mark X.
; APPLICANT: Wells, James A.
; TITLE OF INVENTION: HERGULIN VARIANTS
; FILE REFERENCE: 402E-476112US
; CURRENT APPLICATION NUMBER: US/10/082,747A
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/101,544
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: PCT/US/98/01579
; PRIOR FILING DATE: 1998-02-10
; PRIOR APPLICATION NUMBER: US 08/799,054
; PRIOR FILING DATE: 1997-02-10
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 101
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-082-747A-101

Query Match 85.7%; Score 293; DB 4; Length 56;
Best Local Similarity 96.3%; Pred. No. 7e-27;
Matches 52; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SHLVKAEKERTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYMASFY 54
|||
Db 3 SHLVKAEKERTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYMASFY 56

RESULT 6
US-08-736-019-151
; Sequence 151, Application US/08736019
; Publication No. US20030207799A1
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Marchionni, Mark
; APPLICANT: Chen, Mario
; APPLICANT: Hiles, Ian
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; PREPARATION AND USE
; NUMBER OF SEQUENCES: 189
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Ebling LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible Pentium
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/736, 019
; FILING DATE: 22-OCT-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/471, 833
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036, 555
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965, 173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907, 138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940, 389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863, 703
; FILING DATE: 03-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bleker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200Q
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 428-0200
; TELEFAX: (617) 428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 151:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-736-019-151
Query Match 83.9%; Score 287; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 3,1e-26;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 KCAKEKTFVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYMASFY 54

DB 1 KCAKEKTFVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYMASFY 50
|||||
RESULT 7
US-10-844-218-151
; Sequence 151, Application US/10844218
; Publication No. US20050106666A1
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; Minghetti, Luisa; Waterfield, Michael; Marchionni, Mark;
; Chen, Mario; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; Preparation and Use
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/844, 218
; FILING DATE: 12-AUG-2004
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/036, 555
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: 07/965, 173
; FILING DATE: 23-OCT-1992
; APPLICATION NUMBER: 07/940, 389
; FILING DATE: 03-SEP-1992
; APPLICATION NUMBER: 07/907, 138
; FILING DATE: 30-JUN-1992
; APPLICATION NUMBER: 07/863, 703
; FILING DATE: 03-APRIL-1992
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 151:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 151:
US-10-844-218-151
Query Match 83.9%; Score 287; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 3,1e-26;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 KCAKEKTFVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYMASFY 54
DB 1 KCAKEKTFVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYMASFY 50
|||||
RESULT 8
US-10-082-747A-111
; Sequence 111, Application US/10082747A
; Publication No. US20030129688A1

```
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ APPLICANT: Ballinger, Marcus D.
/ APPLICANT: Jones, Jennifer T.
/ APPLICANT: Fairbrother, Wayne J.
/ APPLICANT: Sliwkowski, Mark X.
/ APPLICANT: Wells, James A.
/ TITLE OF INVENTION: HEREGULIN VARIANTS
/ FILE REFERENCE: 402E-476112US
/ CURRENT APPLICATION NUMBER: US/10/082,747A
/ PRIOR FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: US 09/101,544
/ PRIOR FILING DATE: 1998-07-17
/ PRIOR APPLICATION NUMBER: PCT/US/98/01579
/ PRIOR FILING DATE: 1998-02-10
/ PRIOR APPLICATION NUMBER: US 08/799,054
/ NUMBER OF SEQ ID NOS: 116
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 111
/ LENGTH: 56
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-082-747A-111

Query Match      83.9%; Score 287; DB 4; Length 56;
Best Local Similarity 92.6%; Pred. No. 3,5e-26;
Matches 50; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy
1 SHLVKCAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONQYVM 54
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3 SHLVKCAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONQYVM 56

RESULT 9
/ US-10-096-241-14
/ Sequence 14, Application US/10096241
/ Publication No. US20020127594A1
/ GENERAL INFORMATION:
/ APPLICANT: Geating, David P.
/ TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
/ AND USES THEREFOR
/ NUMBER OF SEQUENCES: 33
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson P.C.
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: US
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/096,241
/ FILING DATE: 12-Mar-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/699,591
/ FILING DATE: 19-AUG-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Faase, J. Peter
/ REGISTRATION NUMBER: 32,983
/ REFERENCE/DOCKET NUMBER: 07334/022001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-542-5070
/ TELEFAX: 617-542-8906
/ TELEX: <Unknown>
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
```

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/ LENGTH: 50 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-096-241-14

Query Match      83.6%; Score 286; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.1e-26;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
1 SHLVKCAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONQYVM 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 SHLVKCAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONQYVM 50

RESULT 10
/ US-10-899-227-14
/ Sequence 14, Application US/10899227
/ Publication No. US20040265970A1
/ GENERAL INFORMATION:
/ APPLICANT: Geating, David P.
/ TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
/ AND USES THEREFOR
/ NUMBER OF SEQUENCES: 33
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson P.C.
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: US
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/899,227
/ FILING DATE: 26-Jul-2004
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/10/096,241
/ FILING DATE: 12-Mar-2002
/ APPLICATION NUMBER: 08/699,591
/ FILING DATE: 19-AUG-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Faase, J. Peter
/ REGISTRATION NUMBER: 32,983
/ REFERENCE/DOCKET NUMBER: 07334/022001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-542-5070
/ TELEFAX: 617-542-8906
/ TELEX: <Unknown>
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 50 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-899-227-14

Query Match      83.6%; Score 286; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.1e-26;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
1 SHLVKCAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONQYVM 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 SHLVKCAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONQYVM 50
```

RESULT 11
US-10-082-747A-96

```

; Sequence 96, Application US/10082747A
; Publication No. US20030129688A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ballinger, Marcus D.
; APPLICANT: Jones, Jennifer T.
; APPLICANT: Fairbrother, Wayne J.
; APPLICANT: Sliwkowski, Mark X.
; APPLICANT: Wells, James A.
; TITLE OF INVENTION: HERGULIN VARIANTS
; FILE REFERENCE: 402E-476112US
; CURRENT APPLICATION NUMBER: US/10/082,747A
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/101,544
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: PCT/US/98/01579
; PRIOR FILING DATE: 1998-02-10
; PRIOR APPLICATION NUMBER: US 08/799,054
; PRIOR FILING DATE: 1997-02-10
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 96
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-082-747A-96

```

Query Match 82.5%; Score 282; DB 4; Length 56;
Best Local Similarity 90.7%; Pred. No. 1,4e-25;
Matches 49; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 SHLVCAEKEKTFVNGGECFVMDLNSPSRYLCKCPNEFTGDRCONVYMASFY 54
Db 3 SHLVCAEKEKTFVNGGECFVMDLNSPSRYLCKCPNEFTGDRCONVYMASFY 56

RESULT 12
US-10-082-747A-108

```

; Sequence 108, Application US/10082747A
; Publication No. US20030129688A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ballinger, Marcus D.
; APPLICANT: Jones, Jennifer T.
; APPLICANT: Fairbrother, Wayne J.
; APPLICANT: Sliwkowski, Mark X.
; APPLICANT: Wells, James A.
; TITLE OF INVENTION: HERGULIN VARIANTS
; FILE REFERENCE: 402E-476112US
; CURRENT APPLICATION NUMBER: US/10/082,747A
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/101,544
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: PCT/US/98/01579
; PRIOR FILING DATE: 1998-02-10
; PRIOR APPLICATION NUMBER: US 08/799,054
; PRIOR FILING DATE: 1997-02-10
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 108
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-082-747A-108

```

Query Match 81.6%; Score 279; DB 4; Length 56;
Best Local Similarity 88.9%; Pred. No. 3,1e-25;
Matches 46; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 SHLVCAEKEKTFVNGGECFVMDLNSPSRYLCKCPNEFTGDRCONVYMASFY 54
Db 3 SHLVCAEKEKTFVNGGECFVMDLNSPSRYLCKCPNEFTGDRCONVYMASFY 56

RESULT 13
US-09-817-647-15

```

; Sequence 15, Application US/09817647
; Patent No. US20020082229A1
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
; TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/817,647
; FILING DATE: 26-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/107,979
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Conley, Delirdre L.
; REGISTRATION NUMBER: 36,487
; REFERENCE/DOCKET NUMBER: P1084R1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-2066
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; FEATURE:
; NAME/KEY: hHRGbeta.egf
; LOCATION: 1-48
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-817-647-15

```

Query Match 81.0%; Score 277; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 4,5e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HLVCAEKEKTFVNGGECFVMDLNSPSRYLCKCPNEFTGDRCONVY 49
Db 1 HLVCAEKEKTFVNGGECFVMDLNSPSRYLCKCPNEFTGDRCONVY 48

RESULT 14
US-09-877-665-15

```

; Sequence 15, Application US/09877665
; Patent No. US20020164680A1
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
; TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
US-09-877-665-15

```

STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,665
FILING DATE: 08-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/109,206
FILING DATE: 30-Jun-1998
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Delidre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
FEATURE:
NAME/KEY: bHRGbeta.egf
LOCATION: 1-48
IDENTIFICATION METHOD:
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-877-665-15

Query Match 81.0%; Score 277; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.5e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HLVKAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYV 49
DB 1 HLVKAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYV 48

RESULT 15
US-10-136-573A-15
Sequence 15, Application US/10136573A
Publication No. US20020161200A1
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Zhang, Melanie Rose
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related Ligands and
TITLE OF INVENTION: Uses therefor
FILE REFERENCE: P1084R1C2
CURRENT APPLICATION NUMBER: US/10/136,573A
CURRENT FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: US 09/480,977
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: US 08/899,437
PRIOR FILING DATE: 1997-07-24
PRIOR APPLICATION NUMBER: US 60/052,019
PRIOR FILING DATE: 1997-07-09
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 15
LENGTH: 48
TYPE: PRT
ORGANISM: Homo sapiens
US-10-136-573A-15

Query Match 81.0%; Score 277; DB 4; Length 48;

Best Local Similarity 100.0%; Pred. No. 4.5e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HLVKAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYV 49
DB 1 HLVKAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYV 48

Search completed: January 26, 2006, 12:54:15
Job time : 114 secs

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OM protein - protein search, using sw model

Run on: January 26, 2006, 12:44:03 ; Search time 32 Seconds

(Without alignments)
20.643 Million cell updates/sec

Title: US-09-980-672-2

Perfect score: 342
Sequence: 1 SHLVKAEKEKTEPCVNGSEC.....GDRQNVMAFYKAEELTY 61

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 45467

Minimum DB seq length: 0
Maximum DB seq length: 61

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88.5	25.9	53	US-11-172-610-5	Sequence 5, Appli
2	87.5	25.6	53	US-11-172-610-7	Sequence 7, Appli
3	77.5	22.7	53	US-11-172-610-2	Sequence 2, Appli
4	73.5	21.5	48	US-11-172-610-6	Sequence 6, Appli
5	71.5	20.9	52	US-11-172-610-4	Sequence 4, Appli
6	70.5	20.6	52	US-11-172-610-3	Sequence 3, Appli
7	70.5	20.6	53	US-11-074-815-1	Sequence 1, Appli
8	70.5	20.6	53	US-11-172-610-1	Sequence 1, Appli
9	66	19.3	50	US-11-172-610-8	Sequence 8, Appli
10	61.5	18.0	45	US-10-055-877-216	Sequence 216, App
11	61.5	18.0	45	US-10-055-877-217	Sequence 217, App
12	61.5	18.0	45	US-10-055-877-218	Sequence 218, App
13	61.5	18.0	45	US-10-055-877-219	Sequence 219, App
14	48.5	14.2	48	US-11-123-896-405	Sequence 405, App
15	46.5	13.7	29	US-10-945-853-8	Sequence 8, Appli
16	46.5	13.6	36	US-10-957-351-17	Sequence 17, Appli
17	46.5	13.6	37	US-10-957-351-72	Sequence 72, Appli
18	44	12.9	18	US-11-128-059-17	Sequence 17, Appli
19	44	12.9	52	US-11-123-896-123	Sequence 123, App
20	44	12.9	52	US-11-123-896-126	Sequence 126, App
21	43.5	12.7	47	US-11-123-896-126	Sequence 126, App
22	42.5	12.4	47	US-11-123-896-362	Sequence 362, App
23	42.5	12.4	47	US-11-123-896-363	Sequence 363, App
24	42	12.3	47	US-11-123-896-429	Sequence 429, App
25	41.5	12.1	49	US-11-123-896-237	Sequence 237, App

26	41	12.0	33	7	US-11-121-301-53	Sequence 53, Appli
27	41	12.0	34	7	US-11-121-301-14	Sequence 14, Appli
28	41	12.0	35	6	US-10-957-351-112	Sequence 112, App
29	41	12.0	47	7	US-11-123-896-456	Sequence 456, App
30	41	12.0	47	7	US-11-019-711-58	Sequence 58, Appli
31	40	11.7	24	7	US-11-128-059-12	Sequence 12, Appli
32	40	11.7	33	7	US-11-113-424-187	Sequence 187, App
33	40	11.7	33	7	US-11-113-424-188	Sequence 188, App
34	40	11.7	33	7	US-11-121-301-51	Sequence 51, Appli
35	40	11.7	33	7	US-11-121-301-52	Sequence 52, Appli
36	40	11.7	35	6	US-10-957-351-26	Sequence 114, App
37	40	11.7	36	6	US-10-957-351-114	Sequence 57, Appli
38	40	11.7	49	7	US-11-019-711-57	Sequence 62, Appli
39	39.5	11.5	37	7	US-11-068-783-62	Sequence 4, Appli
40	39.5	11.5	58	6	US-10-914-391A-4	Sequence 141, App
41	39	11.4	35	6	US-10-957-351-141	Sequence 8, Appli
42	39	11.4	35	7	US-11-121-301-8	Sequence 417, App
43	39	11.4	47	7	US-11-123-896-417	Sequence 357, App
44	38.5	11.3	47	7	US-11-123-896-157	Sequence 399, App
45	38.5	11.3	47	7	US-11-123-896-399	

ALIGNMENTS

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RESULT 1
US-11-172-610-5
; Sequence 5, Application US/11172610
; Publication No. US20060014690A1
; GENERAL INFORMATION:
; APPLICANT: Bishop, Jeffrey S.
; APPLICANT: Loomis, A. Katrina
; APPLICANT: Monticello, Daniel J.
; APPLICANT: Plenkos, Philip T.
; TITLE OF INVENTION: Epidermal Growth Factor Receptor
; FILE REFERENCE: 3530.1002 US2
; CURRENT APPLICATION NUMBER: US/11/172.610
; PRIOR FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/643,082
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 60/564,471
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Mouse
US-11-172-610-5

Query Match      25.9%; Score 88.5; DB 7; Length 53;
Best Local Similarity 36.6%; Pred. No. 0.00011;
Matches 15; Conservative 7; Mismatches 16; Indels 3; Gaps 1;

QY      6 CAEKETFCVNGGECFVVKDLSNPSRYLCKCPNEFTGDRQ 46
       6 CPSSYDGVCLNGVGMCHIESLDS---YTCNCVIGSYSDRQ 43
Db

RESULT 2
US-11-172-610-7
; Sequence 7, Application US/11172610
; Publication No. US20060014690A1
; GENERAL INFORMATION:
; APPLICANT: Bishop, Jeffrey S.
; APPLICANT: Loomis, A. Katrina
; APPLICANT: Monticello, Daniel J.
; APPLICANT: Plenkos, Philip T.
; TITLE OF INVENTION: Epidermal Growth Factor Receptor
; FILE REFERENCE: 3530.1002 US2
; CURRENT APPLICATION NUMBER: US/11/172.610

```

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:
:
: CURRENT FILING DATE: 2005-06-30
: PRIOR APPLICATION NUMBER: 60/643,082
: PRIOR FILING DATE: 2005-01-11
: PRIOR APPLICATION NUMBER: 60/584,471
: PRIOR FILING DATE: 2004-06-30
:
: NUMBER OF SEQ ID NOS: 12
:
: SOFTWARE: FastSeq for Windows Version 4.0.
:
: SEQ ID NO 7
:
: LENGTH: 53
:
: TYPE: prt
:
: ORGANISM: Rat
:
: JS-11-172-610-7

```

Query Match	25.6%;	Score 87.5;	DB 7;	Length 53;
Best Local Similarity	35.7%;	Pred. No. 0.00014;		
Matches 15;	Conservative	8;	Mismatches 16;	Indels

```

QY      6 CAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRQN 47
      |  ::|||  |  ::  |||  |  ::|||  :
Db      6 CPSPYDGYCLNGGVCMYVESV--DRVVCNCVIGYIGERQH 44

```

```

RESULT 3
US-11-172-610-2
/ Sequence 2, Application US/11172610
/ Publication No. US20060014690A1
/ GENERAL INFORMATION:
/ APPLICANT: Bishop, Jeffrey S.
/ APPLICANT: Loomis, A. Katrina
/ APPLICANT: Monticello, Daniel J.
/ APPLICANT: Plenkof, Philip T.
/ TITLE OF INVENTION: Epidermal Growth Factor Receptor
/ TITLE OF INVENTION: Antagonists and Methods of Use
/ FILE REFERENCE: 3530.1002 US2
/ CURRENT APPLICATION NUMBER: US/11/172,610
/ CURRENT FILING DATE: 2005-06-30
/ PRIOR APPLICATION NUMBER: 60/643,082
/ PRIOR FILING DATE: 2005-01-11
/ PRIOR APPLICATION NUMBER: 60/584,471
/ PRIOR FILING DATE: 2004-06-30
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: FaastSEQ for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 53
/ TYPE: PRT
/ ORGANISM: Pig
US-11-172-610-2

```

Query Match	22.7%	Score	77.5	DB	7	Length	53
Best Local Similarity	27.9%	Pred	No. 0.0024				
Matches	12	Conservative	17	Indels	3	Gaps	1

```

QY      5 KCAEKEKTFVCVNGGECFMVYDLSNPSRYLCKCPNEFTGRCON 47
      1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
      ::::| |:::| | | | | | | | | | | | | | | |
DB      5 ECPPSHDGYCLHGVCMYIEAVDS--YACNCVFGYVGERCOH 44
      1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

```

```

RESULT 4
US-11-172-610-6
; Sequence 6, Application US/11172610
; Publication No. US20060014690A1
; GENERAL INFORMATION:
; APPLICANT: Bielop, Jeffrey S.
; APPLICANT: Loomis, A. Katrina
; APPLICANT: Monticello, Daniel J.
; APPLICANT: Plenkos, Philip T.
; TITLE OF INVENTION: Epidermal Growth Factor Receptor
; TITLE OF INVENTION: Antagonists and Methods of Use
; FILE REFERENCE: 3530.1002 US2
; CURRENT APPLICATION NUMBER: US/11/172,610
; CURRENT FILING DATE: 2005-06-30
; PRIORITY APPLICATION NUMBER: 60/643,082
; PRIOR FILING DATE: 2005-01-11

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```

? PRIOR APPLICATION NUMBER: 60/584,477
?
? FRIOR FILING DATE: 2004-06-30
? NUMBER OF SEQ ID NOS: 12
? SOFTWARE: FASTSEQ for Windows Version 1.0
?
? SEQ ID NO: 6
? LENGTH: 48
? TYPE: PRN
? ORGANISM: Horse
JS-11-172-610-6

```

Query Match	21.5%;	Score	73.5;	DB	7;	Length	48;
Best Local Similarity	25.6%;	Pred. No.	0	0068;			
Matches	11;	Conservative	13;	Mismatches	16;	Indels	3;
						Gaps	1;

```
QY      5 KCAEKEKTFVANGGECEFWKDLSPSRYLCKPCNFEFTGRCON 47
Db      5 ECSQSYDGYCLHGKCVYLQVDT--HACNCVVGIVERCOH 44
```

```

RESULT 5
US-11-172-610-4
Sequence 4, Application US/11172610
Publication No. US2006000146S0A1
GENERAL INFORMATION:
APPLICANT: Bishop, Jeffrey S.
APPLICANT: Loomis, A. Katrina
APPLICANT: Monticello, Daniel J.
APPLICANT: Plentkos, Philip T.
TITLE OF INVENTION: Epidermal Growth Factor Receptor
TITLE OF INVENTION: Antagonists and Methods of Use
FILE REFERENCE: 3530.1002 US2
CURRENT APPLICATION NUMBER: US/11/172,610
CURRENT FILING DATE: 2005-06-30
PRIOR APPLICATION NUMBER: 60/643,082
PRIOR FILING DATE: 2005-01-11
PRIOR APPLICATION NUMBER: 60/584,471
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ. ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 52
TYPE: PRT
ORGANISM: Dog
US-11-172-610-4

```

Query Match	20.9%	Score	71.5	DB	7	Length	52
Best Local Similarity	27.9%	Pred. No.	0	013			
Matches	12	Conservative	9	Mismatches	19	Indels	3
						Gaps	1

```
QY      5 KCAEKEKTFVCVNGGECFMYKDLSNPSRYLCKPCNEFTGDRCQN 47
       ::::| | | | | | | | | | | | | | | | | | | | | | :
Db      5 ECPSSYDGYCLYNGVCMYTEAV---DRYACNCVFGEYVGGERCQH 44
```

```

RESULT 6
US-11-172-610-3
; Sequence 3, Application US/11/172610
; Publication No. US200600044650A1
; GENERAL INFORMATION:
; APPLICANT: Bishop, Jeffrey S.
; APPLICANT: Loomis, A. Katrina
; APPLICANT: Monticello, Daniel J.
; APPLICANT: Plentcos, Philip T.
; TITLE OF INVENTION: Epidermal Growth Factor Receptor
; TITLE OF INVENTION: Antagonists and Methods of Use
; FILE REFERENCE: 3530.1002 US2
; CURRENT APPLICATION NUMBER: US/11/172,610
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/643,082
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 60/584,471
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 12

```



```

: SOFTWARE: FASTSQ for Windows Version 4.0.
: SEQ ID NO 3
: LENGTH: 52
: TYPE: PRF
: ORGANISM: Cat
US-11-172-610-3

```

Query Match	20.6%	Score	70.5	DB	7	Length	52
Best Local Similarity	27.9%	Pred.	0.017				
Matches	12	Conservative	9	Mismatches	19	Indels	3
						Gaps	1

Oy 5 KCAEKETPCVNGGECFMYADLSNPSRYLCKCPNEFTGRCON 47
 ::|::|||::|::|::|:
Dd 5 ECPPSYDGYCLYNGVCMTIEAV--DRYACNCVFgygvercqh 44

```

RESULT 7
US-11-074-815-1
; Sequence 1, Application US/11074815
; Publication No. US20050275799A1
; GENERAL INFORMATION:
; APPLICANT: Ocular Sciences, Inc.
; APPLICANT: Mammo, Christopher
; TITLE OF INVENTION: Contact lenses, package systems, and method for promoting a
; TITLE OF INVENTION: healthy epithelium of an eye
; FILE REFERENCE: D-4118
; CURRENT APPLICATION NUMBER: US/11/074,815
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: 60/551,834
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 53
; TYPE: PRN
; ORGANISM: Homo sapiens
; US-11-074-815-1

```

Query Match	20.6%	Score 70.5	DB 7	Length 53
Best Local Similarity	28.6%	Pred. No. 0.018		
Matches 12, Conservative		9, Mismatches 18,	Indels 3,	Gaps 1.

Oy 5 KCAEKEKTFVCVNGGECFMVKDLSNPSRYLCKCPNEFTGRQ 46
 :: :: | : : :
Db 5 ECPPLSHDGYCLHDGVCMYIAL--DKYACNCVVGIYGERQ 43

```

US-11-172-610-1
RESULT 8
; Sequence 1, Application US/11172610
; Publication No. US20060014690A1
; GENERAL INFORMATION:
; APPLICANT: Bishop, Jeffrey S.
; APPLICANT: Loomis, A. Katrina
; APPLICANT: Monticello, Daniel J.
; APPLICANT: Plenkos, Philip T.
; TITLE OF INVENTION: Epidermal Growth Factor Receptor
; TITLE OF INVENTION: Antagonists and Methods of Use
; FILE REFERENCE: 3530.1002 US2
; CURRENT APPLICATION NUMBER: US/11/172,610
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/643,082
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 60/584,471
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-172-610-1

```

Query Match	20.6%	Score	70.5	DB	7	Length	53
Best Local Similarity	28.6%	Pred. No.	0.018				
Matches	12	Conservative	9	Mismatches	18	Indels	3
						Gaps	1

QY 5 KCAEKEKTFVNGGECFPMVKDLSNPSRYLCKCPNEFTGDRCQ 46
 ::: | | :: | : | |
DB 5 ECPRLSHDGYCLHDGVCMYLIAL--DKYACNCVVGTIGERCQ 43

```

RESULT 9
US-11-172-610-8
; Sequence 8, Application US/11172610
; Publication No. US200600014690A1
; GENERAL INFORMATION:
; APPLICANT: Bishop, Jeffrey S.
; APPLICANT: Loomis, A. Katrina
; APPLICANT: Monticello, Daniel J.
; APPLICANT: Plenkof, Philip T.
; TITLE OF INVENTION: Epidermal Growth Factor Receptor
; TITLE OF INVENTION: Antagonists and Methods of Use
; FILE REFERENCE: 3530.1002 US2
; CURRENT APPLICATION NUMBER: US/11/172,610
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/643,082
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 60/584,471
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FaelsSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-11-172-610-8

```

Query Match	19.3%	Score 66:	DB 7:	Length 50:
Best Local Similarity	27.7%	Pred. No.	0.059:	
Matches 13:	Conservative 10:	Mismatches 20:	Indels 4:	Gaps 1:

Oy

1 SHLVKAEKEKTFVANGGECFMVKDLSNPSRYLCKPCNEFTGDRCQN 47
|| : ||| : | : ||| :
Dd 3 SHENDCPDSHTQFCFHGTGRFLVQE---DKPACVCCHSGYVGARCEH 45

RESULT 10
US-10-055-877-216
Sequence 216, Application US/10055877
Publication No. US20050288241A1
GENERAL INFORMATION:
APPLICANT: Decistofaro, Marc
APPLICANT: Padigaru, Muralidhara
APPLICANT: Miller, Charles
APPLICANT: Tchernev, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Gerlach, Valerie
APPLICANT: Spytek, Kimberly
APPLICANT: Ratelli, Luca
APPLICANT: Kekuda, Ramesh
APPLICANT: Guo, Xiaojia
APPLICANT: zernhusen, Bryan
APPLICANT: Andrew, David
APPLICANT: Mezes, Peter
APPLICANT: Patuturajan, Meera
APPLICANT: Burgess, Catherine
APPLICANT: Aisen, Andrew
APPLICANT: Wolenc, Adam
APPLICANT: Baumgartner, Jason
APPLICANT: Shmukets, Richard
APPLICANT: Gusev, Vladimir

```

; APPLICANT: Vermet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 216
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EGF domain
; US-10-055-877-216

Query Match      18.0%; Score 61.5; DB 6; Length 45;
Best Local Similarity 38.5%; Pred. No. 0.19; 15; Indels 7; Gaps 2;
Matches 15; Conservative 2; Mismatches 15;

QY      14  CVNGGECFMVKDLS--NPSRYLCKCPN-----EFTGDRG 45
Db      7  CSNGGTCVNTPGGSSDNFGYTCECPGDDYLYLSTGKRC 45

RESULT 11
US-10-055-877-217
; Sequence 217, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tcherenev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zernhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera

```

```

; APPLICANT: Burgess, Catherine
; APPLICANT: Bisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vermet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 217
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EGF domain
; US-10-055-877-217

Query Match      18.0%; Score 61.5; DB 6; Length 45;
Best Local Similarity 38.5%; Pred. No. 0.19; 15; Indels 7; Gaps 2;
Matches 15; Conservative 2; Mismatches 15;

QY      14  CVNGGECFMVKDLS--NPSRYLCKCPN-----EFTGDRG 45
Db      7  CSNGGTCVNTPGGSSDNFGYTCECPGDDYLYLSTGKRC 45

RESULT 12
US-10-055-877-218
; Sequence 218, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tcherenev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca

```

APPLICANT: Kekuda, Rameesh
APPLICANT: Guo, Xiaojia
APPLICANT: Zetnussen, Bryan
APPLICANT: Andrew, David
APPLICANT: Mezes, Peter
APPLICANT: Patturajan, Meera
APPLICANT: Burgess, Catherine
APPLICANT: Eisen, Andrew
APPLICANT: Wolenc, Adam
APPLICANT: Baumgartner, Jason
APPLICANT: Shinkets, Richard
APPLICANT: Gusev, Vladimir
APPLICANT: Vernet, Corine
APPLICANT: Taupier Jr., Raymond
APPLICANT: Pena, Carol
APPLICANT: Shenoy, Suresh
APPLICANT: Li, Li
APPLICANT: Casman, Stracie
APPLICANT: Boldog, Ferenc
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251
CURRENT APPLICATION NUMBER: US/10/055,877
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/262,892
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263,598
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/263,799
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,139
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,478
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/263,351
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/272,870
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/275,990
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/275,927
PRIOR FILING DATE: 2001-03-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 512
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 218
LENGTH: 45
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: EGF domain
US-10-055-877-218

Query Match 18.0%; Score 61.5; DB 6; Length 45;
Best Local Similarity 38.5%; Pred. No. 0.19;
Matches 15; Conservative 2; Mismatches 15; Indels 7; Gaps 2;

QY 14 CVMGECMVDLS--NPSRYLCKCPN-----EFTGDRG 45
DB 7 CSMGTCTVTPGGSSDNFGYTCBCPPGDYLYLSTGKRC 45

RESULT 13
US-10-055-877-219
Sequence 219, Application US/10055877
Publication No. US20050288241A1
GENERAL INFORMATION:
APPLICANT: Decristofaro, Marc
APPLICANT: Padigaru, Muralidhara
APPLICANT: Miller, Charles
APPLICANT: Tchiernev, Velizar

APPLICANT: Zhong, Mei
APPLICANT: Anderson, David
APPLICANT: Baillinger, Robert
APPLICANT: Gerlach, Valerie
APPLICANT: Spytek, Kimberly
APPLICANT: Ratelli, Luca
APPLICANT: Kekuda, Rameesh
APPLICANT: Guo, Xiaojia
APPLICANT: Zetnussen, Bryan
APPLICANT: Andrew, David
APPLICANT: Mezes, Peter
APPLICANT: Patturajan, Meera
APPLICANT: Burgess, Catherine
APPLICANT: Eisen, Andrew
APPLICANT: Wolenc, Adam
APPLICANT: Baumgartner, Jason
APPLICANT: Shinkets, Richard
APPLICANT: Gusev, Vladimir
APPLICANT: Vernet, Corine
APPLICANT: Taupier Jr., Raymond
APPLICANT: Pena, Carol
APPLICANT: Shenoy, Suresh
APPLICANT: Li, Li
APPLICANT: Casman, Stracie
APPLICANT: Boldog, Ferenc
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251
CURRENT APPLICATION NUMBER: US/10/055,877
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/262,892
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263,598
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/263,799
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PRIOR APPLICATION NUMBER: 60/264,117
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PRIOR APPLICATION NUMBER: 60/264,139
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PRIOR APPLICATION NUMBER: 60/264,478
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/263,351
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/272,870
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/275,990
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/275,927
PRIOR FILING DATE: 2001-03-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 512
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 219
LENGTH: 45
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: EGF domain
US-10-055-877-219

Query Match 18.0%; Score 61.5; DB 6; Length 45;
Best Local Similarity 38.5%; Pred. No. 0.19;
Matches 15; Conservative 2; Mismatches 15; Indels 7; Gaps 2;

QY 14 CVMGECMVDLS--NPSRYLCKCPN-----EFTGDRG 45
DB 7 CSMGTCTVTPGGSSDNFGYTCBCPPGDYLYLSTGKRC 45

RESULT 14
US-11-123-896-405
Sequence 405, Application US/11123896

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/ Publication No. US20050273881A1
/ GENERAL INFORMATION:
/ APPLICANT: Simmons, Carl R.
/ APPLICANT: Navarro Acevedo, Pedro A.
/ APPLICANT: Harvell, Leslie
/ APPLICANT: Cahoon, Rebecca
/ APPLICANT: McCutchen, Billy Fred
/ APPLICANT: Lu, Albert
/ APPLICANT: Hermann, Rafael
/ APPLICANT: Wong, James
/ TITLE OF INVENTION: Defensin Polynucleotides and Methods of
/ FILE REFERENCE: 35718/246703
/ CURRENT APPLICATION NUMBER: US/11/123,896
/ PRIOR FILING DATE: 2005-05-06
/ PRIOR APPLICATION NUMBER: 60/300,152
/ PRIOR FILING DATE: 2001-06-22
/ PRIOR APPLICATION NUMBER: 60/300,241
/ PRIOR FILING DATE: 2001-06-22
/ NUMBER OF SEQ. ID NOS: 469
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 405
/ LENGTH: 48
/ TYPE: PRT
/ ORGANISM: Rictinus communis
US-11-123-896-405
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Query Match      14.2%; Score 48.5; DB 7; Length 48;
Best Local Similarity 23.9%; Pred. No. 8.1;
Matches 11; Conservative 6; Mismatches 16; Indels 13; Gaps 2;
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QY      6 CAEKEKTF---CVNGGECFMVYKDLSPSRYLCKCPNEFTGDRCONV 48
Db      3 CESKSHHFHGPCLRDHNCALV-----CRTEGNFSGGRCRGF 38
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RESULT 15
US-10-945-853-8
/ Sequence 8, Application US/10945853
/ Publication No. US2005025517A1
/ GENERAL INFORMATION:
/ APPLICANT: Biogen, Inc.
/ APPLICANT: Sanicola-Nadel, Michele
/ APPLICANT: Adkins, Heather
/ APPLICANT: Miklasz, Steven Donald
/ APPLICANT: Rayhorn, Paul
/ APPLICANT: Schiffer, Susan Gail
/ APPLICANT: Williams, Kevin
/ TITLE OF INVENTION: Cipro-Specific Antibodies
/ FILE REFERENCE: BGN117CPCCN
/ CURRENT APPLICATION NUMBER: US/10/945,853
/ CURRENT FILING DATE: 2004-09-20
/ PRIOR APPLICATION NUMBER: PCT/US02/31462
/ PRIOR FILING DATE: 2002-10-01
/ PRIOR APPLICATION NUMBER: PCT/US02/11950
/ PRIOR FILING DATE: 2002-04-17
/ PRIOR APPLICATION NUMBER: 60/286,782
/ PRIOR FILING DATE: 2001-04-26
/ PRIOR APPLICATION NUMBER: 60/293,020
/ PRIOR FILING DATE: 2001-05-17
/ PRIOR APPLICATION NUMBER: 60/301,091
/ PRIOR FILING DATE: 2001-06-26
/ PRIOR APPLICATION NUMBER: 60/367,002
/ PRIOR FILING DATE: 2002-03-22
/ NUMBER OF SEQ. ID NOS: 9
/ SEQ ID NO 8
/ LENGTH: 29
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: Mod_res
/ LOCATION: 1
/ OTHER INFORMATION: N-terminal acetylation
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US-10-945-853-8

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Query Match      13.7%; Score 47; DB 6; Length 29;
Best Local Similarity 28.6%; Pred. No. 7.6;
Matches 10; Conservative 4; Mismatches 13; Indels 8; Gaps 1;
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QY      15 VNGGECFMVYKDLSPSRYLCKCPNEFTGDRCONV 49
Db      1 LNEGTCLGS-----FCACPPSFYGRNCEHDV 27
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Search completed: January 26, 2006, 12:54:58
Job time : 33 secs